

178167

From: Whiteman, Brian
Sent: Tuesday, January 31, 2006 12:55 PM
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10/725,013

SEQ ID NO: 2

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Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

Searcher: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
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Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:45:13 ; Search time 16 Seconds
(without alignments)
420.385 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 1 MLGVLVIGALALAGLGPAP.....APSKVVLQHVTRTERPQL 574

Sequence: 3203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	631	US-10-995-561-546	Sequence 546, App
2	587.5	18.3	652	US-10-821-234-1016	Sequence 1016, App
3	426	13.3	1664	US-10-055-877-212	Sequence 212, App
4	414.5	12.9	1574	US-10-055-877-211	Sequence 211, App
5	411	12.8	1620	US-10-055-877-213	Sequence 213, App
6	386	12.1	1198	US-10-453-372-880	Sequence 880, App
7	386	12.1	1398	US-10-055-877-46	Sequence 46, App
8	386	12.1	1398	US-10-453-372-872	Sequence 872, App
9	386	12.1	1450	US-10-055-877-48	Sequence 48, App
10	386	12.1	1450	US-10-453-372-874	Sequence 874, App
11	386	12.1	1594	US-10-453-372-860	Sequence 860, App
12	384	12.0	2871	US-11-169-041-131	Sequence 131, App
13	384	12.0	3002	US-10-821-234-916	Sequence 916, App
14	379.5	11.8	1403	US-10-055-877-52	Sequence 52, App
15	379.5	11.8	1403	US-10-453-372-878	Sequence 878, App
16	379.5	11.8	1404	US-10-055-877-44	Sequence 44, App
17	379.5	11.8	1404	US-10-453-372-870	Sequence 870, App
18	379.5	11.8	1547	US-10-453-372-886	Sequence 886, App
19	379.5	11.8	1577	US-10-055-877-54	Sequence 54, App
20	379.5	11.8	1577	US-10-453-372-882	Sequence 882, App
21	379.5	11.8	1577	US-10-453-372-884	Sequence 884, App
22	379.5	11.8	1620	US-10-453-372-868	Sequence 868, App
23	379.5	11.8	1653	US-10-453-372-866	Sequence 866, App
24	373	11.6	1418	US-10-453-372-864	Sequence 864, App
25	358.5	11.2	956	US-11-113-424-39	Sequence 39, App

26	350	10.9	915	US-10-131-826A-294	Sequence 294, App
27	348.5	10.9	1902	US-10-453-372-1004	Sequence 1004, App
28	337.5	10.5	999	US-11-113-424-36	Sequence 36, App
29	335	10.5	993	US-11-137-465-36	Sequence 36, App
30	332.5	10.4	997	US-11-080-991-50	Sequence 50, App
31	332.5	10.4	4495	US-10-453-372-1002	Sequence 1002, App
32	330.5	10.3	897	US-11-137-465-35	Sequence 35, App
33	328	10.2	961	US-11-113-424-35	Sequence 35, App
34	325	10.1	1400	US-10-821-234-1045	Sequence 1045, App
35	323	10.1	965	US-11-113-424-2	Sequence 2, App
36	322	10.1	964	US-11-137-465-58	Sequence 58, App
37	322	10.1	965	US-11-147-047-51	Sequence 51, App
38	321	10.0	443	US-10-131-826A-318	Sequence 318, App
39	315	9.8	602	US-10-453-372-1064	Sequence 1064, App
40	313.5	9.8	997	US-11-113-424-37	Sequence 37, App
41	310.5	9.7	703	US-10-821-234-1412	Sequence 1412, App
42	296.5	9.3	387	US-11-137-465-57	Sequence 57, App
43	295	9.2	493	US-11-169-041-157	Sequence 157, App
44	295	9.2	497	US-10-821-234-1119	Sequence 1119, App
45	280.5	8.8	2471	US-11-050-346-68	Sequence 68, App

ALIGNMENTS

RESULT 1
US-10-995-561-546
; Sequence 546, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARIGLIU, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-546

Query Match	99.2%	Score 3176.5	DB 6	Length 631
Best Local Similarity	99.5%	Pred. No. 1.2e-215		
Matches	572	Conservative	0	Mismatches 2; Indels 1; Gaps 1;
Q	1	MLGVLVIGALALAGLGPAPPEPQPGSQCEHDCFPALYGPATFTLNASQICDGLRGHLM	60	
D	57	MLGVLVIGALALAGLGPAPPEPQPGSQCEHDCFPALYGPATFTLNASQICDGLRGHLM	116	
Q	61	TVRSVADVLSLLINDGGVRRRLWIGLQIPGCGDKRLGRLGFRQVWVGDNNTSYS	120	
D	117	TVRSVADVLSLLINDGGVRRRLWIGLQIPGCGDKRLGRLGFRQVWVGDNNTSYS	176	
Q	121	RMARLDNGAPLGPCLVAVSAARATVSPRIWEQCCYKAGSFLCEHFPPATCRPLAV	180	
D	177	RMARLDNGAPLGPCLVAVSAARATVSPRIWEQCCYKAGSFLCEHFPPATCRPLAV	236	
Q	181	EPGAAVAASITVGTTPPARAGDFQALPVSSAAVADLGLQIMCTAPGAVOGHMAEAP	240	
D	237	EPGAAVAASITVGTTPPARAGDFQALPVSSAAVADLGLQIMCTAPGAVOGHMAEAP	296	
Q	241	GAMDCSYENGCGEHCNAIPGARPCCPAGALQADGRSCTAS-TGSCNDLCEHFVCPNP	299	
D	297	GAMDCSYENGCGEHCNAIPGARPCCPAGALQADGRSCTAS-TGSCNDLCEHFVCPNP	356	
Q	300	DQPSYSYCMETGRIAADHRCEDVDDCTLESPGCRQVUNVQGGEGECYPRYDLDVG	359	
D	357	DQPSYSYCMETGRIAADHRCEDVDDCTLESPGCRQVUNVQGGEGECYPRYDLDVG	416	

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Qy 360 ECVBPVDFCFRANCEYOCQPLNQTSLVCVCAEGFAP1PHEBHRCOMFCNQACPADCDPN 419
| | | | |
Db 417 ECVBPVDFCFRANCEYOCQPLNQTSLVCVCAEGFAP1PHEBHRCOMFCNQACPADCDPN 476
| | | | |
Qy 420 TQASCCEBEGYILDDGFCTDIDCEGNGFSGVCHNLPGTFECICGPDALARIHIGTDC 479
| | | | |
Db 477 TQASCCEBEGYILDDGFCTDIDCEGNGFSGVCHNLPGTFECICGPDALARIHIGTDC 536
| | | | |
Qy 480 DSGVDDGSDSGSGRPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
| | | | |
Db 537 DSGVDDGSDSGSGRPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 596
| | | | |
Qy 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPORL 574
| | | | |
Db 597 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPORL 631
| | | | |

RESULT 2
; Sequence 1016, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_version 1.0
; SEQ ID NO 1016
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1016

Query Match 18.3%; Score 587.5; DB 6; Length 652;
Best Local Similarity 31.5%; Pred. No. 2,7e-34;
Matches 179; Conservative 57; Mismatches 210; Indels 123; Gaps 31;

Qy 2 LGVILVIGALALA--GLGPPAPAPQPGSGQVCHNDFALYPPTATFLNASTQICDGLRHTL 59
| | | | |
Db 5 MCLLLLLLLLLLTOPGAGTGADTE---AVVCVGTACTYHSGKLSAAEQNHNCNNGSGL 60
| | | | |
Qy 60 MIVRSVAVAD----VLSLLNDGCVGR--RLMTGLQLPFG--CGDPKRLGLRGPOWT 112
| | | | |
Db 61 ATVKSRKEAQRVQRYLAQLLRREALTAMSKFHWGLQREKCKLDPSL--PLKGFHWG 118
| | | | |
Qy 113 GNNNTSYSMWRLDNGAPLGLCVVA--VSAEATVPSE--PIWEBOC-----EVKAD 163
| | | | |
Db 119 GSEDTPIYSWMKELNNSC--ISKRCVSLDLDSQLPLRLKMSBPGSGSPGNSNIE 176
| | | | |
Qy 164 GFLCFHPPATCRPLAV--EPGAAAAVSTTGTTPPAAGDQALPVSSAAVAPLGLQL 222
| | | | |
Db 177 GFVCFSPFGMCRPLALGPRG-----QVTTYTPFTTSSLEAVFPASAAVVA----- 224
| | | | |
Qy 223 MC-TAPPGAVQGHM--AREAPGAM-----CSVENGGCHAC--NALPGAR 263
| | | | |
Db 225 -CGEGDKETQSHYFLCKEKAPDVFDWGSSGPLCVSPKVCNFGNGCHQDFEGGDSGF 283
| | | | |
Qy 264 PQCCPGALALQADRGCTASTGSCNLCB--HFCVNPPOPGSYSCMCTGYRIADQHR 321
| | | | |
Db 284 LCGCRGRFLDLDTVCASRNPCSSSPCGGATCVLGP--HGKNTCRCPQGQGLDSSQLD 342
| | | | |
Qy 322 CEDVDCLIEPSPCPORCVNTQGFCHCYPNYDLVDSGCEVPVDFCFRANCEYOCQPLN 381
| | | | |
Db 343 CVDVDECC--QDSFCAQBCVNTBGFRCCEWVG-----EGGCF-----GGGACQDND 387
| | | | |
Qy 382 QTSYLCVCAEGFAP1PHEBHRCOMFCNQACPADCDPNQAS--CECPBEGYIL--DDGFI 437
| | | | |
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Db 388 E-----CALGRSP-----CAQGC--TNTDGSFRCCEBEGYVLAGBDGTQ 424
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Qy 438 CTDIDEC--ENGFCGSGVCHNLPGTFECICGPDALARIHIGTDCSGKV-----DG 486
| | | | |
Db 425 CQDVDECVGGGGLCQSLCQNTGSGFHCGLPCWVLAIPN--GVACTMGVPVSLGPPSGPPDE 483
| | | | |
Qy 487 GDSGSGE-----PPSPPTGSLTPPA 508
| | | | |
Db 484 EDKKEKSGTVPPRAATASPTRGPGETPKA 512
| | | | |

RESULT 3
; Sequence 212, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernov, Vellizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zethusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eichen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkels, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Sureeh
; APPLICANT: Li, Li
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Renecce
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 212
 LENGTH: 1664
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-10-055-877-212

Query Match 13.3%; Score 426; DB 6; Length 1664;
 Best Local Similarity 27.7%; Pred. No. 1,4e-22;
 Matches 138; Conservative 49; Mismatches 200; Indels 112; Gaps 23;

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QY YSRMARLDNGAPLGGPLCVAVSAAB-----ATPSPPIHEBOOE--VAADGLGCF 169
DB 56 YLRFRPSRRGSKCCLLRQANCSADLCNGGTCPSSHNDNEQVCECPVFTAKCY 115
QY 170 HEPATCPPLAVPAGAAAVSITTYGTPFARGADQALPVSSAAVAPLGLQIMCTAPG 229
DB 116 D-ANNC--MANNCGHEHCYN--TIGTY-----CRCWPG 145
QY 230 AVQGHMABAPGAMDCSVENGGCEHAQNAIPGAPPCQCPAGAAQADGRSC----- 280
DB 146 FELSGDGNWCSIDIDCAVANGGCSDRCVNSPGFRCDCPSDLYLHADGRTCGSGHFENL 205
QY 281 -----TASTQSCNDLCHEFCVNPDPQSGYSCKMCTGYRLADQHRCEVDYDCIIPSPRC 335
DB 206 ILIKKVTSCSTDNGGCEHC--ENDSNGEFYRCRCVGFPLSKNKSQPVDPDFNKGQC 264
QY 336 FORCVNTQGFECFCYPNYDL--VDGECVEPVPDPCFRAN--CEYQCCPLNQTSTLCVCASEG 393
DB 265 QHCHNNHGRACQCYPGFHLSYDRSCVDIDCKANNCGHEFCENVKGT--YRCKCRSEY 323
QY 394 APIPEHRCQMF-----CNQTPACPADC--DENTQASCECPGYLL--DGFICTDIDSC- 444
DB 324 -QLGRDGRTECEMLGGCQVANGGCGHDCDQDGDGHVCKCRNGYLLANDQKLCHDINEH 382
QY 445 ENGCGSCVCANLPCTFECTICPDSALAHITG-----DCSGKVDG-----DSGSGEP 494
DB 383 ENNGDCSQICVNLASVBCQCKPGLMKDRKTCBDISCSN--NGGEGQICSNQEGGY 440
QY 495 PPSPTGSTLPFPVAVG-----LVHSGLLIGISTASLCVVALALALCHLKKQGAAR- 546
DB 441 MCSCEPFGELSDGSHCDNAECLINNG-----GCAQLC-----KNRKGSRRC 483
QY 547 -----AKMEYKCAAPS 557
DB 484 QCFAGYILAHDEKSCVAAS 502

RESULT 4
US-10-055-877-211
; Sequence 211, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernyev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zetunuen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard

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; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-055-877-211

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Query Match 12.9%; Score 414.5; DB 6; Length 1574;
 Best Local Similarity 34.2%; Pred. No. 8,4e-22;
 Matches 104; Conservative 28; Mismatches 101; Indels 71; Gaps 17;

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QY 224 CTAPPG-AVQGHMAREAGANDCSVENGGCEHACHAATIGARPCQCPAGAAQADGRSCTA 282
DB 147 CRCPGYQLQGD--GTCQDVDECRANNGCQHRVCNTPGYSYLCECKPGFRLHTDERTCLA 205
QY 283 STQSC--NDCHEFCVP-----NPDQPGSYSCM----- 308
DB 206 -ISSCTLANGGCQHCQVQLTYTQHRCCQRPQYQLQEDGRRCVRRNSPCAEHGGCMAHIOE 264
QY 309 -----CETGYRLADQHRCEVDYDCILPSPPCPCVNTQGGFECFCYPNYDL--VDG 359
DB 265 LRGLAHGCHHGYQLAADARKTCEDVDSCALGLAQAHGCLNTQGSFKVCVAGYELGADG 324
QY 360 -EC---VEPYDPCFRAN--CEYQCCPLNQTSTLCVCAEGFAPLPIHEHRCQMF----- 407
DB 325 RQCYRIEMEIYNSCEAGNGGCSHGCSH--TSTGPLCTCPRGY-----ELDEQKTCIDIDD 378
QY 408 --NOTACPADDDPNTQA--SCECPGYLLD--DGFICTDIDSCENG--GFCSGVCNHLPGTF 461
DB 379 CANSPPCCQAC-AVTPGYSCTPAGYRLNTDGGCGCEVDDECAQSHGGCEHHCSNLAASF 437
QY 462 ECIC 465
DB 438 QCFC 441

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RESULT 5
 US-10-055-877-213
 ; Sequence 213, Application US/10055877

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/ Publication No. US20050286241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchiernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Rytelk, Kimberly
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eiseen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Sureeh
/ APPLICANT: Li, Li
/ APPLICANT: Caeman, Stacie
/ APPLICANT: Boldog, Ference
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
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/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 213
/ LENGTH: 1620
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-055-877-213

Query Match      12.8%; Score 411; DB 6; Length 1620;
Best Local Similarity 25.9%; Pred. No. 1.5e-21;
Matches 142; Conservative 47; Mismatches 197; Indels 162; Gaps 25;
```

```

/ Publication No. US20060003323A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsebrook, et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-589 A
/ CURRENT APPLICATION NUMBER: US/10/453,372
/ CURRENT FILING DATE: 2003-06-03
/ PRIOR APPLICATION NUMBER: 09/789390
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/185967
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/823187
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/195792
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: 09/839446
/ PRIOR FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 60/199476
/ PRIOR FILING DATE: 2000-03-25
/ PRIOR APPLICATION NUMBER: 09/863776
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: 60/208263
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: 09/93398
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/227800
/ PRIOR FILING DATE: 2000-08-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1609
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 880
/ LENGTH: 1198
/ TYPE: PRT
/ ORGANISM: Homo sapiens

Db      116 D-ANEC--MANNGCHEHCVA--TIGTY-----CRCWPG 145
Qy      230 AVQGHMAREAPGADSCVENGCHEACNAIPGAPCCCPAGAAIADGRSCTASTGSC-- 287
Db      146 FELSGDNTGSDIDIECAVNSGCGSDRCVNSPGGRCPCPSDLYLHADGRTCGYT-SCST 204
Qy      288 -NDLCHEFCVPNPQPSYSQCMCTGYRLAADQRCEDVDCLIEPSPCPQRCVNTGGGF 346
Db      205 DNGGCEHC--ENDSNGEFCRCRCVGFKLSENKRSQPVPCFDNKGCGQHCTNNHGRA 263
Qy      347 ECHGCPYVDL-VDEGCEVPEVPCFRAN-CEYQCOPLNQTSTYLCVCAEGFAPIPHEPRQC 404
Db      264 QCCCTPGFHLSYDRSCVDIDIECAKNNGCHEHCENAVGT-YRCRCREGY-QLGSDARTCE 321
Qy      405 MF-----CNOTACPADC--DPTQASCECEGYTL----- 432
Db      322 EMLGGCQVNGGCGCHDCYDQPDGSHVCKRNGYLLANDQKLCNDNISSTVTHARARLWDS 381
Qy      433 -----DDGF-----ICTDIDEC-ENGFCSGVCH 455
Db      382 YEIVTCVPTDITLTCMKMLDSGHVOCFCDDGYELIDSKFCODINCHENNQDSCSIQCV 441
Qy      456 NLPGTFPCIGSPDSALARIHT-----DCDSGKYDGG-----DSGSGEPSPPTPGSTLT 505
Db      442 NLAGSVBQCKPGRFLMKDRKTCIDISCSN--NGGCBQICSNQBGCMSCBEPFELS 499
Qy      506 PPAVG-----LVHSGLLIGISIASLCLVVALALALCHLRKKQGAAR-----AKM 549
Db      500 EDGHSCHDMNECLINN-----GCAQLC-----KNRGSRRCCQCFAGYLLAHD 542
Qy      550 EYKCAAPG 557
Db      543 EKSCVAAS 550

RESULT 6
US-10-453-372-880
/ Sequence 880, Application US/10453372
/ Publication No. US20060003323A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsebrook, et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-589 A
/ CURRENT APPLICATION NUMBER: US/10/453,372
/ CURRENT FILING DATE: 2003-06-03
/ PRIOR APPLICATION NUMBER: 09/789390
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/185967
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/823187
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/195792
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: 09/839446
/ PRIOR FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 60/199476
/ PRIOR FILING DATE: 2000-03-25
/ PRIOR APPLICATION NUMBER: 09/863776
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: 60/208263
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: 09/93398
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/227800
/ PRIOR FILING DATE: 2000-08-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1609
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 880
/ LENGTH: 1198
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```


;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: curaseqlist version 0.1
;; SEQ ID NO 872
;; LENGTH: 1398
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-872

Query Match 12.1%; Score 386; DB 6; Length 1398;

Best Local Similarity 33.8%; Pred. No. 7.4e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;

QY 224 CTAPRGAVQGMAREAPAMPCSVNNGGCEHACNAIPARPCQCPAGAAADAGRSCTAS 283
DB 143 CHCEPG-FQG--PRCQYDVDCRTHNGGCGHRCVNTPGSYLCECKPGRFLHTDSRTCLA- 198
QY 284 TQSC---NDLCEHFV-----PNDPQGS----- 304
DB 199 INSCALNGSGQHHCYQVLTIRHRCQCRPGQLDGDHNCVRSPCANRNSCMHRCQV 258
QY 305 --YSCMCEGYRLAADGRCEDVDCTLEBSPQRCVNTQGGEGHCYENYDL-VDG- 359
DB 259 RGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGCINTQGSFKVCVCHAGYELGADGR 318
QY 360 EC---VERVDPCEPRAN--CEYQCPPLNQTYS--LCVCAEGPAPIPHBP--RCOMFCNQ 409
DB 319 QCYRIEMIVNSCEANNNGCSHG---SHTSAGPLCTCPRGYELDTDRTICRRLCRQ 375
QY 410 TACPADCDPNTQA--SCECEPGYILD-DGFICTDIDECENG--GFCSGVCHNLPGTFECTIC 465
DB 376 PVLQGVCTNNPGGEGCGCYAGYRLSADCGCEDVDECASSRGCGCHHCTNLAGSFQCGC 434

RESULT 9

US-10-055-877-48

Sequence 48, Application US/10055877

Publication No. US20050288241A1

GENERAL INFORMATION:

;; APPLICANT: Decristofaro, Marc
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Miller, Charles
;; APPLICANT: Tchierney, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Ratelli, Luca
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Guo, Xiaojia
;; APPLICANT: Zernusen, Bryan
;; APPLICANT: Andrew, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patturajan, Weera
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Eileen, Andrew
;; APPLICANT: Wolenc, Adam
;; APPLICANT: Baumgartner, Jason
;; APPLICANT: Shinkets, Richard
;; APPLICANT: Gusev, Vladimir
;; APPLICANT: Vernet, Corine
;; APPLICANT: Taupier Jr., Raymond
;; APPLICANT: Pena, Carol
;; APPLICANT: Shenoy, Suresh
;; APPLICANT: Li, Li
;; APPLICANT: Caeman, Stacie
;; APPLICANT: Boldog, Ferenc
;; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;; FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10/055,877

;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 48
;; LENGTH: 1450
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-48

Query Match 12.1%; Score 386; DB 6; Length 1450;

Best Local Similarity 33.8%; Pred. No. 7.7e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;

QY 224 CTAPRGAVQGMAREAPAMPCSVNNGGCEHACNAIPARPCQCPAGAAADAGRSCTAS 283
DB 143 CHCEPG-FQG--PRCQYDVDCRTHNGGCGHRCVNTPGSYLCECKPGRFLHTDSRTCLA- 198
QY 284 TQSC---NDLCEHFV-----PNDPQGS----- 304
DB 199 INSCALNGSGQHHCYQVLTIRHRCQCRPGQLDGDHNCVRSPCANRNSCMHRCQV 258
QY 305 --YSCMCEGYRLAADGRCEDVDCTLEBSPQRCVNTQGGEGHCYENYDL-VDG- 359
DB 259 RGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGCINTQGSFKVCVCHAGYELGADGR 318
QY 360 EC---VERVDPCEPRAN--CEYQCPPLNQTYS--LCVCAEGPAPIPHBP--RCOMFCNQ 409
DB 319 QCYRIEMIVNSCEANNNGCSHG---SHTSAGPLCTCPRGYELDTDRTICRRLCRQ 375
QY 410 TACPADCDPNTQA--SCECEPGYILD-DGFICTDIDECENG--GFCSGVCHNLPGTFECTIC 465
DB 376 PVLQGVCTNNPGGEGCGCYAGYRLSADCGCEDVDECASSRGCGCHHCTNLAGSFQCGC 434

RESULT 10

US-10-453-372-874

Sequence 874, Application US/10453372

Publication No. US2006000323A1

GENERAL INFORMATION:

;; APPLICANT: Alsobrook, et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-589 A
;; CURRENT APPLICATION NUMBER: US/10/453,372
;; CURRENT FILING DATE: 2003-06-03
;; PRIOR APPLICATION NUMBER: 09/789390
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/823187
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195792


```
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: CuroSeqList version 0.1
;; SEQ ID NO: 874
;; LENGTH: 1450
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-874
```

```
Query Match 12.1%; Score 386; DB 6; Length 1450;
Best Local Similarity 33.8%; Pred. No. 7,7e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;
```

```
QY 224 CTAPPGAVQGHWAAREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGSSCTAS 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 CHCPFG-FQG--PRCQYDVDECRTHNGGCGQHRCVNTPGSYLCECKRPFRLHTDSRTCLA- 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 TQSC---NDLCEHFCV-----PNDQPGS----- 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 INSCALGNGGCGQHCVQLTTRHRCQCRPGFQLQEDGRHCVRRSPCANRNGSCMRQCV 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 ---VSCMCEGYRLADQHRCEVDVDCILBSPFCQRCVNTQGGFECCHPYVDL-VDG- 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 RGLARCEHVGQLADQKACEDVDECAAGLAQCHAGCLINTQGSFKVCYCHAGYELGADGR 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 EC---VEVPDPCFRAN--CEYQCPPLNQTST--LCVCAEGFAPLPHEPH--RCOMFCNQ 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 QCYRIEMEIIVNSCEANNNGGCSHG---SHTSAGPLCTCPRGVELTDDRTICRRLCRQ 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 TACPADCPNTOA-SCEPBEYILD-DGFICTDIDECENG-GFGSGVCHNLPETRECTIC 465
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 PVLQGVCTNNPGYEGCGYAGYRLSADGCGCEDVDECCASSRGCCHHCTNLNLAGSFQSC 434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 11
US-10-453-372-860
;; Sequence 860, Application US/10453372
;; Publication No. US2006000323A1
;; GENERAL INFORMATION:
;; APPLICANT: Alsbrook, et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-589 A
;; CURRENT FILING DATE: US/10/453,372
;; PRIOR APPLICATION NUMBER: 09/789390
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/823187
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195792
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
```

```
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: CuroSeqList version 0.1
;; SEQ ID NO: 860
;; LENGTH: 1594
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-860
```

```
Query Match 12.1%; Score 386; DB 6; Length 1594;
Best Local Similarity 33.8%; Pred. No. 8,5e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;
```

```
QY 224 CTAPPGAVQGHWAAREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGSSCTAS 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 CHCPFG-FQG--PRCQYDVDECRTHNGGCGQHRCVNTPGSYLCECKRPFRLHTDSRTCLA- 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 TQSC---NDLCEHFCV-----PNDQPGS----- 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 INSCALGNGGCGQHCVQLTTRHRCQCRPGFQLQEDGRHCVRRSPCANRNGSCMRQCV 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 ---VSCMCEGYRLADQHRCEVDVDCILBSPFCQRCVNTQGGFECCHPYVDL-VDG- 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 RGLARCEHVGQLADQKACEDVDECAAGLAQCHAGCLINTQGSFKVCYCHAGYELGADGR 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 EC---VEVPDPCFRAN--CEYQCPPLNQTST--LCVCAEGFAPLPHEPH--RCOMFCNQ 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 QCYRIEMEIIVNSCEANNNGGCSHG---SHTSAGPLCTCPRGVELTDDRTICRRLCRQ 379
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 TACPADCPNTOA-SCEPBEYILD-DGFICTDIDECENG-GFGSGVCHNLPETRECTIC 465
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 PVLQGVCTNNPGYEGCGYAGYRLSADGCGCEDVDECCASSRGCCHHCTNLNLAGSFQSC 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 12
US-11-169-041-131
;; Sequence 131, Application US/11169041
;; Publication No. US20060019284A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;; TITLE OF INVENTION: CELLS
;; FILE REFERENCE: 10001 NP
;; CURRENT APPLICATION NUMBER: US/11/169,041
;; CURRENT FILING DATE: 2005-06-28
;; PRIOR APPLICATION NUMBER: 60/584,405
;; PRIOR FILING DATE: 2004-06-30
;; NUMBER OF SEQ ID NOS: 527
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO: 131
;; LENGTH: 2871
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-169-041-131
```

```
Query Match 12.0%; Score 384; DB 7; Length 2871;
Best Local Similarity 29.0%; Pred. No. 2,1e-19;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;
```

```
QY 244 DCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTASTQSCNDLCEHFCVNP----- 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1200 ECSINNGGCEFTCNSEGSYSCSCOPFALMPDQRSCT-----DIDE--CEDNPNICD 1250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 -----DQGSYSQMCCEGYRLADQHRCEVDVDCILBSPFC-QRCVNTQGGFECCHCYPN 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1251 GGQCTNIPGEYRCLCYGFMASBDMKTCVDVNECDLMPNICTLSTGTCENTKGSFTCHDMG 1310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
Qy 354 YDLVDGE--CYPEVDPC--FRANCEYOCQPLNQT-SYLCVCAEGFA-----PIPH 398
Db 1311 YSGKKGKGTCTD-INCEIIGHNCGKHAVCTNTAGSFKCSGSPMIGDICTDLDECNS 1369
Qy 399 EPHRCQMFQNTACPADCDPTQAS--CECEGYILLDDGFICTDIDEC-EN-----446
Db 1370 GTHMCSQH-----ADC-KNTMGSYRCLCKEgy-TGDFCTCTDLDECSENLNLCGNGQC 1420
Qy 447 ---GGF-----CS-----GVCHNLPGTEFCICGPPSALAR 473
Db 1421 LNAEGIRCECDMGFVPBSADKACEDIECSLPNLCVGTCHNLPGLRCCEIGYELDR 1480
Qy 474 HIG-----TDCSGKVDGDSGSGEPSPSPGS-----TLTPAVGLV- 512
Db 1481 SGNCTDVNECLDPTTCTISGNCVN-----TPGSYICDCPPDFELNPTRVGCV 1528
Qy 513 -HSG-----LLIGISIASLCLVALLALCHLRKQGA-----A 545
Db 1529 TRSGNCYLDIRPRGDNBDTACSNELGVGVSRASCC-----CSLCKAGTPEMCPA 1579
Qy 546 RAKMEYKCAAPSK-----VYLQHV 565
Db 1580 VNTSEYKILCPGSGFRPNPTVILEDI 1607

RESULT 13
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Suean
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC SEQ_genes Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPR: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916

Query Match 12.0%; Score 384; DB 6; Length 3002;
Best Local Similarity 29.0%; Pred. No. 2,2e-19;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;

Qy 244 DCSVENGCEHACNAIPGARPCQCPAGALQADGSSCTASTOSCNLDLCEHFCVPPN- 299
Db 1331 ECSINWGGCEFFCTNSGSEYECSCQPGFALMPDORSCT-----DIDE--CEDPNICD 1381
Qy 300 -----DQGSYSQMETGYRLAADHRCEDVDDCLLEBPC--PQCVNQGGECHCYCN 353
Db 1382 GGQCTNIGERYCLCTDYGFMASEDMKTCVNECDLNPTICSGTCENTKGSFICHDMG 1441
Qy 354 YDLVDGE--CYPEVDPC--FRANCEYOCQPLNQT-SYLCVCAEGFA-----PIPH 398
Db 1442 YSGKKGKGTCTD-INCEIIGHNCGKHAVCTNTAGSFKCSGSPMIGDICTDLDECNS 1500
Qy 399 EPHRCQMFQNTACPADCDPTQAS--CECEGYILLDDGFICTDIDEC-EN-----446
Db 1501 GTHMCSQH-----ADC-KNTMGSYRCLCKEgy-TGDFCTCTDLDECSENLNLCGNGQC 1551
Qy 447 ---GGF-----CS-----GVCHNLPGTEFCICGPPSALAR 473
Db 1552 LNAEGIRCECDMGFVPBSADKACEDIECSLPNLCVGTCHNLPGLRCCEIGYELDR 1611
Qy 474 HIG-----TDCSGKVDGDSGSGEPSPSPGS-----TLTPAVGLV- 512
```

```
Db 1612 SGNCTDVNECLDPTTCTISGNCVN-----TPGSYICDCPPDFELNPTRVGCV 1659
Qy 513 -HSG-----LLIGISIASLCLVALLALCHLRKQGA-----A 545
Db 1660 TRSGNCYLDIRPRGDNBDTACSNELGVGVSRASCC-----CSLCKAGTPEMCPA 1710
Qy 546 RAKMEYKCAAPSK-----VYLQHV 565
Db 1711 VNTSEYKILCPGSGFRPNPTVILEDI 1738

RESULT 14
US-10-055-877-52
; Sequence 52, Application US/10055877
; Publication No. US2005028241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkels, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Scacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 52
LENGTH: 1403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-52

Query Match 11.8%; Score 379.5; DB 6; Length 1403;
Best Local Similarity 32.3%; Pred. No. 2.1e-19;
Matches 98; Conservative 31; Mismatches 105; Indels 69; Gaps 16;

QY 224 CTAPPGAVQ---GHWAREAPGAMDCSVNCGCEHACNAIPGARPCQCPAGAAALQADGRS 279
DB 146 CRWPPSHQLOQDGETCDVD---ECRTNNGCQHRCVNTPGSYLCECKPGRFRLHTDSRT 202
QY 280 CTASTQSC---NDLCEHFCV-----PNPQPS----- 304
DB 203 C--AINSCALNGGCGQHHCVOQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMR 260
QY 305 -----YSCMCTGYRLADQHRCEVDVDCILBSPPCORCVNTQGFECHCYPNYDL- 356
DB 261 CQVVRGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGLNTQGSFKVCYCHAGYELG 320
QY 357 VDG-EC---VEPVDPCEFRAN--CEYOCQPLNQTYS--LCVCAEGFAPIPHEPH--RCQM 405
DB 321 ADGRQCYRIEMBIIVNSCEANNGCSHG---SHTSAGPLCTCPRGYELDTDQRTICRCR 377
QY 406 FCNQTACPADDDPNTQA--SCCEPBGYILD-DGFICTDIDECENG-GFCSGVCNMLPGTPE 462
DB 378 LCRQPVLOQVCTNNPGYEGCGYAGYRLSADGCGCEDVDECASSRGCGCHHCTNLAGSFQ 437
QY 463 CIC 465
DB 438 CSC 440

RESULT 15

US-10-453-372-878
Sequence 878, Application US/10453372
Publication No. US2006000323A1

GENERAL INFORMATION:

APPLICANT: Alsbodrok, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 878
LENGTH: 1403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-878

Query Match 11.8%; Score 379.5; DB 6; Length 1403;
Best Local Similarity 32.3%; Pred. No. 2.1e-19;
Matches 98; Conservative 31; Mismatches 105; Indels 69; Gaps 16;

QY 224 CTAPPGAVQ---GHWAREAPGAMDCSVNCGCEHACNAIPGARPCQCPAGAAALQADGRS 279
DB 146 CRWPPSHQLOQDGETCDVD---ECRTNNGCQHRCVNTPGSYLCECKPGRFRLHTDSRT 202
QY 280 CTASTQSC---NDLCEHFCV-----PNPQPS----- 304
DB 203 C--AINSCALNGGCGQHHCVOQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMR 260
QY 305 -----YSCMCTGYRLADQHRCEVDVDCILBSPPCORCVNTQGFECHCYPNYDL- 356
DB 261 CQVVRGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGLNTQGSFKVCYCHAGYELG 320
QY 357 VDG-EC---VEPVDPCEFRAN--CEYOCQPLNQTYS--LCVCAEGFAPIPHEPH--RCQM 405
DB 321 ADGRQCYRIEMBIIVNSCEANNGCSHG---SHTSAGPLCTCPRGYELDTDQRTICRCR 377
QY 406 FCNQTACPADDDPNTQA--SCCEPBGYILD-DGFICTDIDECENG-GFCSGVCNMLPGTPE 462
DB 378 LCRQPVLOQVCTNNPGYEGCGYAGYRLSADGCGCEDVDECASSRGCGCHHCTNLAGSFQ 437
QY 463 CIC 465
DB 438 CSC 440

Search completed: February 4, 2006, 04:48:27
Job time : 18 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:44:33 ; Search time 181 Seconds
(without alignments)
1325.050 Million cell updates/sec

Title: US-10-725-013-2
Perfect score: 3203
Sequence: 1 MLGVLVIGALALAGLGFPPAP.....APSKVVLQHVRTERTPQRL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3203	100.0	574	4	US-10-725-013-2
2	3176.5	99.2	575	4	US-10-150-440-3
3	3176.5	99.2	575	4	US-10-373-801-29
4	3176.5	99.2	575	4	US-10-712-124-110
5	3176.5	99.2	575	5	US-10-785-156-2
6	3176.5	99.2	631	4	US-10-150-440-1
7	3176.5	99.2	631	4	US-10-741-601-309
8	3172.5	99.0	575	3	US-09-938-405-2
9	3172.5	99.0	575	4	US-10-438-648-2
10	3172.5	99.0	575	4	US-10-410-195-2
11	3159.5	98.6	575	4	US-10-094-866-196
12	2789.5	87.1	497	4	US-10-298-796-4
13	1323	41.3	239	4	US-10-104-047-2759
14	1219	38.1	224	5	US-10-478-360-1
15	869	27.1	157	5	US-10-478-360-2
16	792.5	24.7	223	3	US-10-478-360-13
17	775.5	24.2	418	4	US-10-427-805-2
18	753	23.5	397	4	US-10-427-805-3
19	695	21.7	127	5	US-10-478-360-4
20	590.5	18.4	645	4	US-10-029-386-3151
21	590.5	18.4	652	4	US-10-408-765A-1422
22	590.5	18.4	652	5	US-10-741-600-1310
23	590.5	18.4	652	5	US-10-741-600-1311
24	590.5	18.4	652	5	US-10-820-155-1
25	590.5	18.4	652	5	US-10-820-155-79
26	588.5	18.4	652	3	US-09-789-919-96
27	587.5	18.3	648	5	US-10-461-862-116

28	587.5	18.3	648	5	US-10-461-862-118	Sequence 118, App
29	587.5	18.3	652	4	US-10-021-660-83	Sequence 83, Appl
30	587.5	18.3	652	4	US-10-211-462-131	Sequence 131, Appl
31	587.5	18.3	652	5	US-10-820-155-82	Sequence 82, Appl
32	587.5	18.3	652	5	US-10-820-155-117	Sequence 117, App
33	578	18.0	467	4	US-10-210-172-176	Sequence 176, App
34	578	18.0	757	3	US-09-918-715-177	Sequence 177, App
35	578	18.0	757	3	US-09-918-715-196	Sequence 196, App
36	578	18.0	757	4	US-10-262-445-107	Sequence 107, App
37	578	18.0	757	4	US-10-712-124-102	Sequence 102, App
38	578	18.0	757	4	US-10-474-794-177	Sequence 177, App
39	578	18.0	757	4	US-10-474-794-196	Sequence 196, App
40	578	18.0	757	5	US-10-723-860-443	Sequence 443, App
41	578	18.0	757	5	US-10-979-159-177	Sequence 177, App
42	578	18.0	757	5	US-10-979-159-196	Sequence 196, App
43	575	18.0	765	3	US-09-918-715-190	Sequence 190, App
44	575	18.0	765	3	US-09-918-715-291	Sequence 291, App
45	575	18.0	765	4	US-10-474-794-190	Sequence 190, App

ALIGNMENTS

RESULT 1
US-10-725-013-2
; Sequence 2, Application US/10725013
; Publication No. US20040196683A1
; GENERAL INFORMATION:
; APPLICANT: Sehgal, Lakshman R.
; TITLE OF INVENTION: Ex vivo and in vivo expression of the thrombomodulin gene
; FILE REFERENCE: 3840-005-27
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/430,099
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-725-013-2

Query Match 100.0%; Score 3203; DB 4; Length 574;
Best Local Similarity 100.0%; Pred. No. 1.1e-209;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLGVLVIGALALAGLGFPPAPBPQSGSCVHDCFALYPPGATPLNLSQICDGLRGHLM	60
DB	1	MLGVLVIGALALAGLGFPPAPBPQSGSCVHDCFALYPPGATPLNLSQICDGLRGHLM	60
QY	61	TVRSVADVLSLLINGDGVGRRRLTWGLQLPCCGDKPLGLRGFWTGDNNTSYS	120
DB	61	TVRSVADVLSLLINGDGVGRRRLTWGLQLPCCGDKPLGLRGFWTGDNNTSYS	120
QY	121	FWARLDLNGALCGPLCAVSAEAETVPSBIWEBOQCEVADGFLCEHFPPATCRPLAV	180
DB	121	FWARLDLNGALCGPLCAVSAEAETVPSBIWEBOQCEVADGFLCEHFPPATCRPLAV	180
QY	181	EPGAAAASVSTTYGPPFAAGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHAREAP	240
DB	181	EPGAAAASVSTTYGPPFAAGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHAREAP	240
QY	241	GAMDCSVENGSCBHAACNAIPGARPCQCPAGALQADGSCSTASTQSCNDLCEHFCVPPND	300
DB	241	GAMDCSVENGSCBHAACNAIPGARPCQCPAGALQADGSCSTASTQSCNDLCEHFCVPPND	300
QY	301	QPGSYSCMCEFGYRLAADQHRCEVDCTLEPSPCPQACVNTQGGFBCHCYPTNDLVNDE	360
DB	301	QPGSYSCMCEFGYRLAADQHRCEVDCTLEPSPCPQACVNTQGGFBCHCYPTNDLVNDE	360

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QY 361 CVEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPHRCOMFCNQTAACPADCDPNT 420
DB 361 CVEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPHRCOMFCNQTAACPADCDPNT 420
QY 421 QASCECEBEGYIILDGFCITDIDECENGGFCGVCCHNLPGTFECTICGPDALARIHIGTDCD 480
DB 421 QASCECEBEGYIILDGFCITDIDECENGGFCGVCCHNLPGTFECTICGPDALARIHIGTDCD 480
QY 481 SGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVVALALLCHLRK 540
DB 481 SGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVVALALLCHLRK 540
QY 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574
DB 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574

RESULT 2
US-10-150-440-3
; Sequence 3, Application US/10150440
; Publication No. US2003002249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Uergen
; APPLICANT: Dzlonek, Andrzej
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; FILE REFERENCE: 212302001200
; CURRENT FILING DATE: US/10/150,440
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-3

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCCTAS-TQSCNDLCEHFCEVNP 299
DB 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCEVNP 300
QY 300 DQPSYSCMCETGYRLAADQRCEDVDCCILEPSPCORCVNTQGFECCHCYPNYDLVDG 359
DB 301 DQPSYSCMCETGYRLAADQRCEDVDCCILEPSPCORCVNTQGFECCHCYPNYDLVDG 360
QY 360 ECVBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPHRCOMFCNQTAACPADCDPN 419
DB 361 ECVBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPHRCOMFCNQTAACPADCDPN 420
QY 420 TQASCECEBEGYIILDGFCITDIDECENGGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 479
DB 421 TQASCECEBEGYIILDGFCITDIDECENGGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 480
QY 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVVALALLCHLR 539
DB 481 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVVALALLCHLR 540
QY 540 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574
DB 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 575

RESULT 3
US-10-373-801-29
; Sequence 29, Application US/10373801
; Publication No. US2004000564A1
; GENERAL INFORMATION:
; APPLICANT: Yibai Pharmaceutical (USA)
; FILE REFERENCE: 12399.00
; CURRENT FILING DATE: US/10/373,801
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-801-29

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 361 ECVEVDVDCFRANCERYCQCPINQTSYLCVCAEGFAPRHEBPRCQPCNQTA CPADCPDN 420
QY 420 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
QY 540 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 574
Db 541 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 575

RESULT 4
US-10-712-124-110
; Sequence 110, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 110
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-110

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHCFALYPGPATFLNASQICDGLRGHLM 60
Db 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHCFALYPGPATFLNASQICDGLRGHLM 60
QY 61 TRSSVADVSTLLNGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Db 61 TRSSVADVSTLLNGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
QY 121 RMARLDLNGAPLCPGLCVAAVSAEATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Db 121 RMARLDLNGAPLCPGLCVAAVSAEATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAANVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHAREAP 240
Db 181 EPGAAAANVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHAREAP 240
QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS-TOSCNDCI:CEHFCVNP 299
Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS-TOSCNDCI:CEHFCVNP 299
QY 300 DQPGSYCMCTGYRLAADQHRCEVDVDCILEPSPCQPCVNTQGFECCHCPYNDLVYG 359
Db 300 DQPGSYCMCTGYRLAADQHRCEVDVDCILEPSPCQPCVNTQGFECCHCPYNDLVYG 359
QY 361 ECVEVDVDCFRANCERYCQCPINQTSYLCVCAEGFAPRHEBPRCQPCNQTA CPADCPDN 420
Db 361 ECVEVDVDCFRANCERYCQCPINQTSYLCVCAEGFAPRHEBPRCQPCNQTA CPADCPDN 420
QY 420 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 420 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
QY 540 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 574
Db 541 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 575

RESULT 5
US-10-785-156-2
; Sequence 2, Application US/10785156
; Publication No. US20050106124A1
; GENERAL INFORMATION:
; APPLICANT: Sehgal, Lakshman R.
; APPLICANT: Wong, Jonathan
; APPLICANT: Seth, Prem
; TITLE OF INVENTION: Therapeutic Applications of Thrombomodulin Gene Via Viral and
; FILE REFERENCE: 3840-006-27
; CURRENT APPLICATION NUMBER: US/10/785,156
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 60/449,408
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-156-2

Query Match 99.2%; Score 3176.5; DB 5; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHCFALYPGPATFLNASQICDGLRGHLM 60
Db 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHCFALYPGPATFLNASQICDGLRGHLM 60
QY 61 TRSSVADVSTLLNGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Db 61 TRSSVADVSTLLNGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
QY 121 RMARLDLNGAPLCPGLCVAAVSAEATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Db 121 RMARLDLNGAPLCPGLCVAAVSAEATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAANVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHAREAP 240
Db 181 EPGAAAANVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHAREAP 240
QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS-TOSCNDCI:CEHFCVNP 299
Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS-TOSCNDCI:CEHFCVNP 299
QY 300 DQPGSYCMCTGYRLAADQHRCEVDVDCILEPSPCQPCVNTQGFECCHCPYNDLVYG 359
Db 300 DQPGSYCMCTGYRLAADQHRCEVDVDCILEPSPCQPCVNTQGFECCHCPYNDLVYG 359
QY 361 ECVEVDVDCFRANCERYCQCPINQTSYLCVCAEGFAPRHEBPRCQPCNQTA CPADCPDN 420
Db 361 ECVEVDVDCFRANCERYCQCPINQTSYLCVCAEGFAPRHEBPRCQPCNQTA CPADCPDN 420
QY 420 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 420 TQASCECEGYTLDDGFICTDIDCEGNGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
QY 540 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 574
Db 540 KKQGAARAKMEYKCAAPSKVEVVLQHVTRTERPQRL 575

```
RESULT 6
US-10-150-440-1
; Sequence 1, Application US/10150440
; Publication No. US2003022249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Ueergen
; APPLICANT: Schmitz, Andrej
; APPLICANT: Dzionek, William
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; TITLE OF INVENTION: A SUBSET OF DENDRITIC CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 212302001200
; CURRENT APPLICATION NUMBER: US/10/150.440
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-1

Query Match      99.2%; Score 3176.5; DB 4; Length 631;
Best Local Similarity 99.5%; Pred. No. 7.8e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1  MGVVLGALALAGLGPAPAPPOGSGQCVENHDCFLALYPGPATFLNASQICDGLRGHLM 60
DB      57  MGVVLGALALAGLGPAPAPPOGSGQCVENHDCFLALYPGPATFLNASQICDGLRGHLM 116
QY      61  TYRSSVAADVLSLLNGDGVGRRRLWIGLQLPFGCGDKRLGRLRGFQWVTGDNNTSYS 120
DB      117 TYRSSVAADVLSLLNGDGVGRRRLWIGLQLPFGCGDKRLGRLRGFQWVTGDNNTSYS 176
QY      121 RWARLDLNGALPCGPLCYAVASAAEATVPSSEPIWEEQCEVADGFLCFHFPRATCRPLAV 180
DB      177 RWARLDLNGALPCGPLCYAVASAAEATVPSSEPIWEEQCEVADGFLCFHFPRATCRPLAV 236
QY      181 EGGAAAAAASITYGPPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 240
DB      237 EGGAAAAAASITYGPPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 296
QY      241 GAMDCSVENGCGEHCNAILPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCVNP 299
DB      297 GAMDCSVENGCGEHCNAILPGARPCQCPAGALQADGSRCTASATQSCNDLCEHFCVNP 356
QY      300 DPGSGYSQCEGTGYRLADQHRCEVDVDCILBSPCPQRCVNTQSGFECGCHCPYNDLVVG 359
DB      357 DPGSGYSQCEGTGYRLADQHRCEVDVDCILBSPCPQRCVNTQSGFECGCHCPYNDLVVG 416
QY      360 ECVPEVDPGCFRANCERYQCPPLNQTSTYLCAEGFAPIPHBPHRCMFCNQTCAPADCDPN 419
DB      417 ECVPEVDPGCFRANCERYQCPPLNQTSTYLCAEGFAPIPHBPHRCMFCNQTCAPADCDPN 476
QY      420 TQASCECPGTYLDDGFICTDIDECENGFGSGVCHNLPGTFEFCICGPDALARRHIGTDC 479
DB      597 TQASCECPGTYLDDGFICTDIDECENGFGSGVCHNLPGTFEFCICGPDALARRHIGTDC 479
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```
RESULT 7
US-10-741-601-309
; Sequence 309, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001500
; CURRENT APPLICATION NUMBER: US/10/741.601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-309

Query Match      99.2%; Score 3176.5; DB 4; Length 631;
Best Local Similarity 99.5%; Pred. No. 7.8e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1  MGVVLGALALAGLGPAPAPPOGSGQCVENHDCFLALYPGPATFLNASQICDGLRGHLM 60
DB      57  MGVVLGALALAGLGPAPAPPOGSGQCVENHDCFLALYPGPATFLNASQICDGLRGHLM 116
QY      61  TYRSSVAADVLSLLNGDGVGRRRLWIGLQLPFGCGDKRLGRLRGFQWVTGDNNTSYS 120
DB      117 TYRSSVAADVLSLLNGDGVGRRRLWIGLQLPFGCGDKRLGRLRGFQWVTGDNNTSYS 176
QY      121 RWARLDLNGALPCGPLCYAVASAAEATVPSSEPIWEEQCEVADGFLCFHFPRATCRPLAV 180
DB      177 RWARLDLNGALPCGPLCYAVASAAEATVPSSEPIWEEQCEVADGFLCFHFPRATCRPLAV 236
QY      181 EGGAAAAAASITYGPPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 240
DB      237 EGGAAAAAASITYGPPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 296
QY      241 GAMDCSVENGCGEHCNAILPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCVNP 299
DB      297 GAMDCSVENGCGEHCNAILPGARPCQCPAGALQADGSRCTASATQSCNDLCEHFCVNP 356
QY      300 DPGSGYSQCEGTGYRLADQHRCEVDVDCILBSPCPQRCVNTQSGFECGCHCPYNDLVVG 359
DB      357 DPGSGYSQCEGTGYRLADQHRCEVDVDCILBSPCPQRCVNTQSGFECGCHCPYNDLVVG 416
QY      360 ECVPEVDPGCFRANCERYQCPPLNQTSTYLCAEGFAPIPHBPHRCMFCNQTCAPADCDPN 419
DB      417 ECVPEVDPGCFRANCERYQCPPLNQTSTYLCAEGFAPIPHBPHRCMFCNQTCAPADCDPN 476
QY      420 TQASCECPGTYLDDGFICTDIDECENGFGSGVCHNLPGTFEFCICGPDALARRHIGTDC 479
DB      477 TQASCECPGTYLDDGFICTDIDECENGFGSGVCHNLPGTFEFCICGPDALARRHIGTDC 536
QY      480 DSGKVDGDSGSGBPSPPTPGSTLTPPAVGLVHSGLLIGISASLCLVVALALLCHLR 539
DB      537 DSGKVDGDSGSGBPSPPTPGSTLTPPAVGLVHSGLLIGISASLCLVVALALLCHLR 596
QY      540 KQGAARARAMEYKCAAPSKYEVLLQHVTERTPQRL 574
DB      597 KQGAARARAMEYKCAAPSKYEVLLQHVTERTPQRL 631
```


RESULT 8

US-09-938-405-2
 ; Sequence 2, Application US/09938405
 ; Patent No. US20020111296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fesicoff, Barry W.
 ; APPLICANT: Morser, Michael J.
 ; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
 ; FILE REFERENCE: 51960AUSM1
 ; CURRENT APPLICATION NUMBER: US/09/938,405
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 60/229,714
 ; PRIOR FILING DATE: 2000-08-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 575
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-938-405-2

Query Match 99.0%; Score 3172.5; DB 3; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1.3e-207;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVTVLGAALAGLGFPAAPAPPOGSGQVCHDCEALYPPATFTLNASQICDGLRGLHM 60
 DB 1 MGVTVLGAALAGLGFPAAPAPPOGSGQVCHDCEALYPPATFTLNASQICDGLRGLHM 60
 QY 61 TVRSSVAADVLSLLNGGSGVGRRLMTGLQLPCCGPKRLGRLRGFWTGDNNNTSYS 120
 DB 61 TVRSSVAADVLSLLNGGSGVGRRLMTGLQLPCCGPKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RWARLDLNGALPGLCPGLCAVAASAEATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDLNGALPGLCPGLCAVAASAEATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAAREAP 240
 DB 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAAREAP 240
 QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 QY 300 DOPGYSVCMCEGTGRLAADQHRCEVDVDCIIEPSPCPORCVNTQGFECCHCYPNYDLVDG 359
 DB 300 DOPGYSVCMCEGTGRLAADQHRCEVDVDCIIEPSPCPORCVNTQGFECCHCYPNYDLVDG 359
 QY 360 ECEVVDPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBHRQMFNCQTACPADCDPN 419
 DB 360 ECEVVDPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBHRQMFNCQTACPADCDPN 419
 QY 420 TQASCECEBYTLLDDGFLCTDIDCEGNGFGSGVCCHNPGTFECICGSDSALARIITGDC 479
 DB 420 TQASCECEBYTLLDDGFLCTDIDCEGNGFGSGVCCHNPGTFECICGSDSALARIITGDC 479
 QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 DB 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 QY 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574
 DB 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574

RESULT 9
 US-10-438-648-2
 ; Sequence 2, Application US/10438648
 ; Publication No. US2003018683A1
 ; GENERAL INFORMATION:

; APPLICANT: Light, David
 ; APPLICANT: Nagashima, Mariko
 ; APPLICANT: Morser, Michael J.
 ; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
 ; FILE REFERENCE: 51863AUSDI
 ; CURRENT APPLICATION NUMBER: US/10/438,648
 ; CURRENT FILING DATE: 2003-05-14
 ; PRIOR APPLICATION NUMBER: US 60/213,678
 ; PRIOR FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: US 09/880,484
 ; PRIOR FILING DATE: 2001-06-12
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 575
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-438-648-2

Query Match 99.0%; Score 3172.5; DB 4; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1.3e-207;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVTVLGAALAGLGFPAAPAPPOGSGQVCHDCEALYPPATFTLNASQICDGLRGLHM 60
 DB 1 MGVTVLGAALAGLGFPAAPAPPOGSGQVCHDCEALYPPATFTLNASQICDGLRGLHM 60
 QY 61 TVRSSVAADVLSLLNGGSGVGRRLMTGLQLPCCGPKRLGRLRGFWTGDNNNTSYS 120
 DB 61 TVRSSVAADVLSLLNGGSGVGRRLMTGLQLPCCGPKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RWARLDLNGALPGLCPGLCAVAASAEATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDLNGALPGLCPGLCAVAASAEATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAAREAP 240
 DB 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAAREAP 240
 QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 QY 300 DOPGYSVCMCEGTGRLAADQHRCEVDVDCIIEPSPCPORCVNTQGFECCHCYPNYDLVDG 359
 DB 300 DOPGYSVCMCEGTGRLAADQHRCEVDVDCIIEPSPCPORCVNTQGFECCHCYPNYDLVDG 359
 QY 360 ECEVVDPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBHRQMFNCQTACPADCDPN 419
 DB 360 ECEVVDPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBHRQMFNCQTACPADCDPN 419
 QY 420 TQASCECEBYTLLDDGFLCTDIDCEGNGFGSGVCCHNPGTFECICGSDSALARIITGDC 479
 DB 420 TQASCECEBYTLLDDGFLCTDIDCEGNGFGSGVCCHNPGTFECICGSDSALARIITGDC 479
 QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 DB 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 QY 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574
 DB 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574

RESULT 10
 US-10-410-195-2
 ; Sequence 2, Application US/10410195
 ; Publication No. US2004002446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fesicoff, Barry W.
 ; APPLICANT: Morser, Michael J.
 ; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
 ; FILE REFERENCE: 51960AUSM1

/ CURRENT APPLICATION NUMBER: US/10/410.195
 / CURRENT FILING DATE: 2003-04-10
 / PRIOR APPLICATION NUMBER: US/09/938, 405
 / PRIOR FILING DATE: 2001-08-23
 / PRIOR APPLICATION NUMBER: 60/229, 714
 / PRIOR FILING DATE: 2000-08-31
 / NUMBER OF SEQ ID NOS: 2
 / SOFTWARE: Patent version 3.1
 / SEQ ID NO 2
 / LENGTH: 575
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-410-195-2

Query Match 99.0%; Score 3172.5; DB 4; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1.3e-207;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 1 MGVTVLGAALAGLGFAPAEPQSGSQVEHDCFPALYPGPATFLNASQICDGLRGHLM 60
DB 1 MGVTVLGAALAGLGFAPAEPQSGSQVEHDCFPALYPGPATFLNASQICDGLRGHLM 60
QY 61 TYRSSVAADVITSLANGGCGVGRRLMTGLQLPFGCGDPKRLGRLRGFWTGDNNTSYS 120
DB 61 TYRSSVAADVITSLANGGCGVGRRLMTGLQLPFGCGDPKRLGRLRGFWTGDNNTSYS 120
QY 121 RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEBOQCEVKADGFLCFHFPPATCRPLAV 180
DB 121 RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEBOQCEVKADGFLCFHFPPATCRPLAV 180
QY 181 BPGAAAAVSTYGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
DB 181 BPGAAAAVSTYGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
QY 241 GAMDQSVENGSGCEHACNAIPGARPCQCPAGALQADGRCSTAS-TQSCNDLCEHFCVPRP 299
DB 241 GAMDQSVENGSGCEHACNAIPGARPCQCPAGALQADGRCSTAS-TQSCNDLCEHFCVPRP 299
QY 300 DQPGSYSCMCTGYTLADQHRCEVDDCITLPSPOPCVNTQGGGFECHCYPNYDLYDG 359
DB 300 DQPGSYSCMCTGYTLADQHRCEVDDCITLPSPOPCVNTQGGGFECHCYPNYDLYDG 359
QY 360 BCVEBVDCCFRANCERYCQPLNQTSLCYCAEGFAPIPHEPRCOMFCNQACPADCDEN 419
DB 360 BCVEBVDCCFRANCERYCQPLNQTSLCYCAEGFAPIPHEPRCOMFCNQACPADCDEN 419
QY 420 TQASCCEPBGTYLIDGFTCTDIDECANGGFCGVCCHNLPGTRECICGPDALVRHIGTDC 479
DB 420 TQASCCEPBGTYLIDGFTCTDIDECANGGFCGVCCHNLPGTRECICGPDALVRHIGTDC 479
QY 480 DSGKVDGSGSGSEPPSPPTPGSTLTPPAVGLVHSGLLIGISASLCLVALLALLCHLR 539
DB 480 DSGKVDGSGSGSEPPSPPTPGSTLTPPAVGLVHSGLLIGISASLCLVALLALLCHLR 539
QY 540 KKGGAARAMEYKCAAPSKKVVLOHVRTERTPQRL 574
DB 540 KKGGAARAMEYKCAAPSKKVVLOHVRTERTPQRL 574
  
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RESULT 11
 US-10-094-886-196
 / Sequence 196, Application US/10094886
 / Publication No. US20040002120A1
 / GENERAL INFORMATION:
 / APPLICANT: Kekuda, Ramesh
 / APPLICANT: Tchernev, Velizar T.
 / APPLICANT: Liu, Xiaohong
 / APPLICANT: Spytek, Kimberly A.
 / APPLICANT: Paturajan, Meera
 / APPLICANT: Burgess, Catherine
 / APPLICANT: Vernet, Corinne A.
 / APPLICANT: Li, Li
 / APPLICANT: Gorman, Linda

```

/ APPLICANT: Malyankar, Uriel M.  

/ APPLICANT: Boldog, Ferenc  

/ APPLICANT: Guo, Xiaojia  

/ APPLICANT: Shenoy, Suresh  

/ APPLICANT: Padigar, Muralidhara  

/ APPLICANT: Taupier, Raymond J., Jr.  

/ APPLICANT: Miller, Charles  

/ APPLICANT: Caeman, Stacie  

/ APPLICANT: Pena, Carol  

/ APPLICANT: Gangolli, Esna  

/ APPLICANT: Gusev, Vladimir  

/ APPLICANT: Smithson, Glenda  

/ APPLICANT: Zethusen, Bryan  

/ APPLICANT: Gerlach, Valerie  

/ APPLICANT: Pochart, Pascal  

/ APPLICANT: Fernandes, Elma  

/ APPLICANT: Shimkess, Richard  

/ APPLICANT: Raetelli, Luca  

/ APPLICANT: Spaderma, Steven  

/ APPLICANT: Larochele, William  

/ APPLICANT: Zhong, Mei  

/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  

/ FILE REFERENCE: 21402-290 B  

/ CURRENT APPLICATION NUMBER: US/10/094, 886  

/ PRIOR APPLICATION NUMBER: 60/274, 322  

/ PRIOR FILING DATE: 2001-03-07  

/ PRIOR APPLICATION NUMBER: 60/313, 182  

/ PRIOR FILING DATE: 2001-08-17  

/ PRIOR APPLICATION NUMBER: 60/288, 052  

/ PRIOR FILING DATE: 2001-05-02  

/ PRIOR APPLICATION NUMBER: 60/318, 510  

/ PRIOR FILING DATE: 2001-09-10  

/ PRIOR APPLICATION NUMBER: 60/274, 281  

/ PRIOR FILING DATE: 2001-03-08  

/ PRIOR APPLICATION NUMBER: 60/314, 018  

/ PRIOR FILING DATE: 2001-08-21  

/ PRIOR APPLICATION NUMBER: 60/274, 194  

/ PRIOR FILING DATE: 2001-03-08  

/ PRIOR APPLICATION NUMBER: 60/274, 849  

/ PRIOR FILING DATE: 2001-03-09  

/ PRIOR APPLICATION NUMBER: 60/296, 693  

/ PRIOR FILING DATE: 2001-06-07  

/ PRIOR APPLICATION NUMBER: 60/313, 626  

/ PRIOR FILING DATE: 2001-08-21  

/ Remaining Prior Application data removed - See file Wrapper or PALM.  

/ NUMBER OF SEQ ID NOS: 298  

/ SOFTWARE: Patentin 2.1  

/ SEQ ID NO 196  

/ LENGTH: 575  

/ TYPE: PRT  

/ ORGANISM: Homo sapiens  

US-10-094-886-196
  
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Query Match 98.6%; Score 3159.5; DB 4; Length 575;
 Best Local Similarity 99.0%; Pred. No. 1e-206;
 Matches 569; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 MGVTVLGAALAGLGFAPAEPQSGSQVEHDCFPALYPGPATFLNASQICDGLRGHLM 60
DB 1 MGVTVLGAALAGLGFAPAEPQSGSQVEHDCFPALYPGPATFLNASQICDGLRGHLM 60
QY 61 TYRSSVAADVITSLANGGCGVGRRLMTGLQLPFGCGDPKRLGRLRGFWTGDNNTSYS 120
DB 61 TYRSSVAADVITSLANGGCGVGRRLMTGLQLPFGCGDPKRLGRLRGFWTGDNNTSYS 120
QY 121 RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEBOQCEVKADGFLCFHFPPATCRPLAV 180
DB 121 RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEBOQCEVKADGFLCFHFPPATCRPLAV 180
QY 181 BPGAAAAVSTYGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
DB 181 BPGAAAAVSTYGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
  
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Qy 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGASCTAS-TQSCNDLCEHFCVBNP 299
Db 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGASCTASATOSCNDCCEHFCVBNP 300
Qy 300 DQPSYSCMCTGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDG 359
Db 301 DQPSYSCMCTGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDG 360
Qy 360 ECVBVDPCFRANCERYOCQPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPN 419
Db 361 ECVBVDPCFRANCERYOCQPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPN 420
Qy 420 TQASCECEGYILDDGFICTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDC 479
Db 421 TQASCECEGYILDDGFICTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDC 480
Qy 480 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
Db 481 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 540
Qy 540 KKQGAARAKMEYKCAAPSKVVLQHVTRERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTRERTPORL 575

RESULT 12

US-10-298-796-4
; Sequence 4, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-4

Query Match 87.1%; Score 2789.5; DB 4; Length 497;
Best Local Similarity 99.2%; Pred. No. 1.3e-181;
Matches 493; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 19 APAPPOPGSGSCVHEDCFALYGPATFLINASQICGLRGLHMTYRASSVAADVISILLNGD 78
Db 1 APAPPOPGSGSCVHEDCFALYGPATFLINASQICGLRGLHMTYRASSVAADVISILLNGD 60
Qy 79 GGVRRRLMIGLQLPBGCGDPKRLGRLGFMVYGDNNNTSYRWRRLDNLGAPLCGPICV 138
Db 61 GGVRRRLMIGLQLPBGCGDPKRLGRLGFMVYGDNNNTSYRWRRLDNLGAPLCGPICV 120
Qy 139 AVSAAEATVPSEPIWEBOOCEVKADGFLCEHFPAFCPLAVEPGAAAASITYGTPFA 198
Db 121 AVSAAEATVPSEPIWEBOOCEVKADGFLCEHFPAFCPLAVEPGAAAASITYGTPFA 180
Qy 199 ARGADFOALPVYSSAAVAPLGIQLMCTAPPGAQVGHMAREAPGAMDCSVENGCCEHACNA 258
Db 181 ARGADFOALPVYSSAAVAPLGIQLMCTAPPGAQVGHMAREAPGAMDCSVENGCCEHACNA 240
Qy 259 IPGARPCQCPAGALQADGASCTAS-TQSCNDLCEHFCVBNPQGGFCHCYPNDLVDG 317
Db 241 IPGARPCQCPAGALQADGASCTASATOSCNDCCEHFCVBNPQGGFCHCYPNDLVDG 300
Qy 318 DQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDGCEVBPVPCFRANCERYOC 377
Db 318 DQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDGCEVBPVPCFRANCERYOC 377

Db 301 DQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDGCEVBPVPCFRANCERYOC 360
Qy 378 QPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEGYILDDGFI 437
Db 361 QPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECEGYILDDGFI 420
Qy 438 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCSGKVDGDSGSGEPSPS 497
Db 421 CTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCSGKVDGDSGSGEPSPS 480
Qy 498 PTPGSTLTPPAVGLVHS 514
Db 481 PTPGSTLTPPAVGLVHS 497

RESULT 13

US-10-104-047-2759
; Sequence 2759, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2759
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2759

Query Match 41.3%; Score 1323; DB 4; Length 239;
Best Local Similarity 89.1%; Pred. No. 3.9e-82;
Matches 238; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

Qy 308 MCEYGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDGCEVBPVDP 367
Db 1 MCEYGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFCHCYPNDLVDGCEVBPVDP 60
Qy 368 CFRANCERYOCQPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECP 427
Db 61 CFRANCERYOCQPLNQTSTYLCVCAEGFAPIPHEPHRCQMFNCQACPADCDPNTQASCECP 118
Qy 428 EGYILDDGFICTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCSGKVDG 487
Db 119 EGYILDDGFICTDIDECENGFCGSGVCHNLPGTFECICGPDALVRHIGTDCSGKVDG 152
Qy 488 DSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCHLRKKQGAARA 547
Db 153 DSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCHLRKKQGAARA 212
Qy 548 KMEYKCAAPSKVVLQHVTRERTPORL 574
Db 213 KMEYKCAAPSKVVLQHVTRERTPORL 239

RESULT 14

US-10-478-360-1
; Sequence 1, Application US/10478360
; Publication No. US20050014220A1
; GENERAL INFORMATION:
; APPLICANT: Conway, Edward M.
; TITLE OF INVENTION: THE LECTIN LIKE DOMAIN OF THROMBOMODULIN
; FILE REFERENCE: DECE70.002APC
; CURRENT APPLICATION NUMBER: US/10/478,360
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/EP02/05727
; PRIOR FILING DATE: 2002-05-24

;; PRIOR APPLICATION NUMBER: EP 01201979.0
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 224
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)...(224)
;; OTHER INFORMATION: Human thrombomodulin fragment 1
US-10-478-360-1

Query Match 38.1%; Score 1219; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,4e-75;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 80
DB 1 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 60
QY 81 VGRRLWATGLQPPGCGPKRLGRLRGFQWTTGDNNTSYSRWARLDLNGAPLCGPLCVAV 140
DB 61 VGRRLWATGLQPPGCGPKRLGRLRGFQWTTGDNNTSYSRWARLDLNGAPLCGPLCVAV 120
QY 141 SAAEATVPSSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAASITYGTFPAAR 200
DB 121 SAAEATVPSSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAASITYGTFPAAR 180
QY 201 GADFOALPVGSSAAVAAPLGLQIMCTAPPAVQGHWAREAPGAMD 244
DB 181 GADFOALPVGSSAAVAAPLGLQIMCTAPPAVQGHWAREAPGAMD 224

RESULT 15
US-10-478-360-2
;; Sequence 2, Application US/10478360
;; Publication No. US20050014220A1
;; GENERAL INFORMATION:
;; APPLICANT: Conway, Edward M.
;; TITLE OF INVENTION: THE LECTIN LIKE DOMAIN OF THROMBOMODULIN
;; TITLE OF INVENTION: AND ITS THERAPEUTIC USE
;; FILE REFERENCE: DEC1E70.002APC
;; CURRENT APPLICATION NUMBER: US/10/478,360
;; CURRENT FILING DATE: 2003-11-21
;; PRIOR APPLICATION NUMBER: PCT/EP02/05727
;; PRIOR FILING DATE: 2002-05-24
;; PRIOR APPLICATION NUMBER: EP 01201979.0
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)...(157)
;; OTHER INFORMATION: Human thrombomodulin fragment 2
US-10-478-360-2

Query Match 27.1%; Score 869; DB 5; Length 157;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 80
DB 1 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 60
QY 81 VGRRLWATGLQPPGCGPKRLGRLRGFQWTTGDNNTSYSRWARLDLNGAPLCGPLCVAV 140
DB 61 VGRRLWATGLQPPGCGPKRLGRLRGFQWTTGDNNTSYSRWARLDLNGAPLCGPLCVAV 120

QY 141 SAAEATVPSSEPIWEQCEVADGFLCEFHFPATCRP 177
DB 121 SAAEATVPSSEPIWEQCEVADGFLCEFHFPATCRP 157

Search completed: February 4, 2006, 04:48:04
Job time : 183 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:24:27 ; Search time 199 Seconds
(without alignments)
1267.354 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MLGVLVIGALALAGLPAP.....APSKKVLQHVTRTPTQL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	575	6	ABG72575 Human chr
2	3176.5	99.2	575	7	ABM78950 Breast ca
3	3176.5	99.2	575	7	ADBS4760 Human Pro
4	3176.5	99.2	575	7	ADD48168 Human Pro
5	3176.5	99.2	575	8	ADN04006 Antipbort
6	3176.5	99.2	575	8	ADP12616 Protein e
7	3176.5	99.2	575	8	ADO28681 Human chr
8	3176.5	99.2	575	8	ADP79506 Human chr
9	3176.5	99.2	575	8	ADP32191 Human chr
10	3176.5	99.2	575	8	ADU06321 Novel bro
11	3176.5	99.2	631	6	ABG72572 Human chr
12	3176.5	99.2	681	8	ADN05602 Antipbort
13	3172.5	99.0	575	2	AAR11534 Human chr
14	3172.5	99.0	575	2	AAR11806 Thrombomo
15	3172.5	99.0	575	2	AAR43031 Human chr
16	3172.5	99.0	575	2	AAE17521 Human chr
17	3172.5	99.0	575	5	AAE23026 Human chr
18	3170.5	99.0	575	1	AAE2070 Human chr
19	3168.5	98.9	575	2	AAE31572 Human chr
20	3163.5	98.8	575	2	AAE20639 Human chr
21	3159.5	98.6	575	6	ABU52408 Human GPC
22	3159.5	98.6	575	8	ADL24151 Human NOV
23	3139.5	98.0	575	2	AAW73970 Human chr
24	3122.5	97.5	575	2	AAR22189 Sequence

25	3083.5	96.3	557	5	AAE17528 Human chr
26	3083.5	96.3	557	5	AAE17525 Human chr
27	3083.5	96.3	557	5	AAE23031 Human chr
28	3083.5	96.3	557	5	AAE23028 Human chr
29	3082.5	96.2	557	5	AAE17523 Human chr
30	3081.5	96.2	557	5	AAE17596 Human chr
31	3080.5	96.2	557	5	AAE17530 Human chr
32	3080.5	96.2	557	5	AAE17538 Human chr
33	3079.5	96.1	557	5	AAE17526 Human chr
34	3079.5	96.1	557	5	AAE23029 Human chr
35	3078.5	96.1	557	5	AAE17593 Human chr
36	3078.5	96.1	557	5	AAE17595 Human chr
37	3078.5	96.1	557	5	AAE17597 Human chr
38	3078.5	96.1	557	5	AAE17529 Human chr
39	3078.5	96.1	557	5	AAE17527 Human chr
40	3078.5	96.1	557	5	AAE23030 Human chr
41	3077.5	96.1	557	5	AAE17592 Human chr
42	3077.5	96.1	557	5	AAE17594 Human chr
43	3077.5	96.1	557	5	AAE17591 Human chr
44	3076.5	96.1	557	5	AAE17524 Human chr
45	3071.5	95.9	554	5	AAE17522 Human chr

ALIGNMENTS

RESULT 1
ABG72575
ID ABG72575 standard; protein, 575 AA.
XX
AC ABG72575;
XX
DT 05-MAR-2003 (first entry)
XX
DE Human thrombomodulin protein #2 (CD141).
XX
KW Human; thrombomodulin; CD141; dendritic cell separation; inflammation;
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; dermatological; cell therapy; dermatomyositis; cancer;
KW autoimmune disorder; rheumatoid arthritis; psoriatic arthritis;
KW alkylosing spondylitis; Sjorgen's syndrome; lupus erythematosus;
KW Goodpasture's syndrome; scleroderma; vasculitis; polymyositis.
XX
OS Homo sapiens.
XX
PN WO200293172-A1.
XX
PD 21-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-US015786.
XX
PR 17-MAY-2001; 2001US-0291561P.
XX
PA (MILT-) MILTENYI BIOTEC INC.
XX
PI Schmitz J, Dzionek A, Buck DW;
XX WPI; 2003-129324/12.
XX
DR Enriching for dendritic cells from a mixture of cells, useful for
XX treating inflammation, cancer or autoimmune disorders such as arthritis,
XX or lupus by contacting the mixture of cell with an antigen-binding
XX fragment specific for CD141.
XX
PS Example 1; Fig 3B; 88pp; English.
PS
XX This invention relates to a novel method for separating dendritic cells
XX from a mixture of cells. The method comprises contacting the mixture of
XX cells with an antigen-binding fragment specific for CD141, and selecting
XX the cells that are CD141 positive therefore producing a dendritic cell-
XX enriched composition. The method of the invention may have
XX antiinflammatory; cytostatic; antiarthritic; antirheumatic;
XX immunosuppressive and dermatological activities and may be used in cell

CC therapy, the methods, compositions and agents of the invention are useful
CC for treating inflammation, cancer or autoimmune disorders such as
CC rheumatoid arthritis, psoriatic arthritis, ankylosing spondylitis,
CC Sjögren's syndrome, lupus erythematosus, Goodpasture's syndrome,
CC scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic
CC cells and populations are useful for screening assays for agents that
CC affect dendritic cell function, and for the phenotypic, functional,
CC biochemical or molecular analyses of dendritic cells. The compositions
CC and dendritic cells are useful as vaccine adjuvants. The present sequence
CC represents a protein sequence of human CD141 protein which is used to
CC generate the dendritic cell specific antibodies that are used in the
CC method of the invention

SQ Sequence 575 AA;

Query Match	99.2%	Score 3176.5	DB 6	Length 575
Similarity	99.5%	Pred. No. 6.1e-175		
Matches 572	Conservative	0	Mismatches 2	Indels 1
				Gaps 1

QY	1	MLGVTVLGA	LALAGLGFAPAPAPQPGSSQCV	EHDCALVPGPATPLNASQICDGLR	GHLM	60					
Db	1	MLGVTVLGA	LALAGLGFAPAPAPQPGSSQCV	EHDCALVPGPATPLNASQICDGLR	GHLM	60					
QY	61	TVRSSVAD	AVISILLINGDGGVGRRLRMIGLQLEP	PGCGDPKRLPLRGFWNTDNN	NTSYS	120					
Db	61	TVRSSVAD	AVISILLINGDGGVGRRLRMIGLQLEP	PGCGDPKRLPLRGFWNTDNN	NTSYS	120					
QY	121	RVARLDLNG	APLCGPLCVAVSAAEATVPSBP	IWEBOQCEVKADGPLCEHF	PATCRPLAV	180					
Db	121	RVARLDLNG	APLCGPLCVAVSAAEATVPSBP	IWEBOQCEVKADGPLCEHF	PATCRPLAV	180					
QY	161	BEGAAAAV	SITTYGTPFAARGADFOLLPVGSS	SAVAAPLGLQIMCTAPRGAVOGH	MAREAP	240					
Db	161	BEGAAAAV	SITTYGTPFAARGADFOLLPVGSS	SAVAAPLGLQIMCTAPRGAVOGH	MAREAP	240					
QY	241	GAMDCSV	ENGCGCEHACNALPGARPCQCP	AGALQADGRSCTAS-TQSCNDL	CEHF	CVPNP					
Db	241	GAMDCSV	ENGCGCEHACNALPGARPCQCP	AGALQADGRSCTAS-TQSCNDL	CEHF	CVPNP					
QY	300	DQPGSYS	CMCETGYRLAADOHRCEVDVDC	ILBPSPCPQRCVNTQGGF	ECH	CYPNYDLVDG					
Db	301	DQPGSYS	CMCETGYRLAADOHRCEVDVDC	ILBPSPCPQRCVNTQGGF	ECH	CYPNYDLVDG					
QY	360	ECVEBEVD	PCFRANCERYQCCPLNQTSLCY	CAEFAPIPHENHNCOMFCNT	ACPADCPN	4139					
Db	361	ECVEBEVD	PCFRANCERYQCCPLNQTSLCY	CAEFAPIPHENHNCOMFCNT	ACPADCPN	420					
QY	420	TQASCECP	RYLLDQFICTDIDECNNGG	CGSVCHNLPTCFBCTCGSP	DALAH	IGTDC					
Db	421	TQASCECP	RYLLDQFICTDIDECNNGG	CGSVCHNLPTCFBCTCGSP	DALAH	IGTDC					
QY	480	DSGKVDG	SGSGSEPPSPPTGSLTLP	PAVGLVHSGLLIGISIAS	LSLTVALLAL	CHLR					
Db	481	DSGKVDG	SGSGSEPPSPPTGSLTLP	PAVGLVHSGLLIGISIAS	LSLTVALLAL	CHLR					
QY	540	KKQGAAR	AMEYKCAAPSKEVVLQHV	RTERTPQRL		574					
Db	541	KKQGAAR	AMEYKCAAPSKEVVLQHV	RTERTPQRL		575					
RESULT 2											
ID	ABM78950	ABM78950 standard; protein; 575 AA.									
XX	ABM78950;										
XX	AC										
DT	15-JAN-2004	(first entry)									
XX	DT										
DE	Breast cancer specific marker under-expressed in breast cancer.										
XX											
KM	Breast cancer; marker; thrombomodulin; human; diagnosis; cytostatic;										
KM	blich1p; vaccline.										
XX											

OS Homo sapiens.
XX WO2003073911-A2.
PN
XX
XX
PD 12-SEP-2003.
XX
XX
PF 27-FEB-2003; 2003WO-US005984.
XX
XX
PR 28-FEB-2002; 2002US-0355999P.
XX
XX
PA (GEOU) UNIV GEORGETOWN.
XX
XX
PI Su YA, Yang J;
XX
XX WPT; 2003-721895/68.
DR N-PsDB; ACF79930.
XX
XX
PT Detecting breast cancer in a subject comprises contacting a biological sample with an agent that binds to a polynucleotide or polypeptide of a breast-cancer specific gene (BCSG).
PS Claim 5, Page 119-121; 143pp; English.

Claim 5; Page 119-121; 143pp; English.

The present sequence is that of a breast cancer specific marker (BCSM)

being under-expressed in breast cancers in comparison to healthy tissue.

coagulation previously reported to be involved in vascular diseases and cancers. It is 1 of 19 (see ABM78941-59) BCsMs of the invention that are

expressed in breast cancer cell lines and breast cancer tissue samples as

provides a method for detection of breast cancer by measuring expression

transcribed from and polypeptides encoded by the BCSGs. A pharmaceutical

agent that modulates an expression level of a BCSG or an activity of a antibody directed against a BCSM, a vaccine generated using a BCSM, or an

inhibit breast cancer comprises a BCSG or BCSM

Sequence 575 AA;

every Match	99.2%	Score 3176.5;	DB 7;	Length 5/5;
at 100% similarity	99.5%	Pred NO 6	1e-175;	

CONSERVATIVE 0; MINIMAL 2; INCREASING 1; CAPS 1

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1. **התאמה בין המסמך לבין המסמך**

61 TPSSVAADYTSIIINGDGCVCBPRIWTGIQIPGCGDPKRIQPIRGFQWYTGDNNTSYS 120

121 RWARLDLNGAPLCGPLCVAVSAEATVPSEPIWEEQCEVKADGFLCEFHFPATCRPLAV 180

121 RWARLDNGAPLCGLCVAVSAEATVPSEPIWEEQQCEVKADGFLCEFHFPATCRPLAV 180

181 EPGAAAAVSITYGTPFAARGADFQALPVGSSAAVAPLGLQIMCTAPPGA VQGHWAREAP 240

181 EPGAAAAVSIITYGTFPAARGADFQALPVSSAAVAPLGLQEMCIAEPGAVQGHMAREAF 240

241 GAMDCS V LINDOCCCEHLCNAT E GNAE CXCZ HOVRNUYRUCNO C ZND

1. **Introduction**

[illegible]

360 ECVEPVDPCEFRANCEYOCPI.NOTSVI.CVCAEGEAPTPHEPHRCOMECONOTACPADCDPN 419

100

Db 361 ECVEVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPRHEPRHRCOMFCNQTRACPADCPN 420

Qy 420 TQASCEBEGYILDDGFICTDIDECENGFCSCGVCHNPGTFECICGPDALARRIGTDC 479

Db 421 TQASCEBEGYILDDGFICTDIDECENGFCSCGVCHNPGTFECICGPDALARRIGTDC 480

Qy 480 DSGKYDGDSDSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 481 DSGKYDGDSDSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540

Qy 540 KKQGAARAKMEYKCAAPSKEVVLQHVRTERTPQRL 574

Db 541 KKQGAARAKMEYKCAAPSKEVVLQHVRTERTPQRL 575

RESULT 3

AD54760

ID AD54760 standard; protein; 575 AA.

XX ADE54760;

AC

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P07204, SEQ ID NO 565.

XX

KM Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

KM spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; F07204.

XX

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX

XX Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIP0 at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 575 AA;

XX

Qy Query Match 99.2%; Score 3176.5; DB 7; Length 575;

Qy Best Local Similarity 99.5%; Pred. No. 6.1e-175;

Qy Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 1 MLGVVLTGALALAGLPAPAPAPOPGSGSCVEHOCFALYPGPATFLNASQICDGLRGLM 60

Db 1 MLGVVLTGALALAGLPAPAPAPOPGSGSCVEHOCFALYPGPATFLNASQICDGLRGLM 60

Qy 61 TVRSSVAADVLSLLNGDGVGRRRLWIGQLPPGCGDPKRLGRLGFOWTGDNNTSYS 120

Db 61 TVRSSVAADVLSLLNGDGVGRRRLWIGQLPPGCGDPKRLGRLGFOWTGDNNTSYS 120

Qy 121 RWARLDLNGAPLCPPLCYAVSAEATVPSSEIWEBOQEVADGFLCEFHPPATCRPLAV 180

Db 121 RWARLDLNGAPLCPPLCYAVSAEATVPSSEIWEBOQEVADGFLCEFHPPATCRPLAV 180

Qy 181 EPGAAAASVITTYGPPFARAGADFOALPVSSAAVAPLGLQIMCTAPGAVQGHMARAP 240

Db 181 EPGAAAASVITTYGPPFARAGADFOALPVSSAAVAPLGLQIMCTAPGAVQGHMARAP 240

Qy 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVENP 299

Db 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVENP 299

Qy 300 DQPGSYSCMCTGTRLAADQRCEDVDDCIIPEPFCPCRCVNTQGFECPCPYNDLVDG 359

Db 300 DQPGSYSCMCTGTRLAADQRCEDVDDCIIPEPFCPCRCVNTQGFECPCPYNDLVDG 359

Qy 360 ECVPEVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPRHEPRHRCOMFCNQTRACPADCPN 419

Db 360 ECVPEVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPRHEPRHRCOMFCNQTRACPADCPN 419

Qy 420 TQASCEBEGYILDDGFICTDIDECENGFCSCGVCHNPGTFECICGPDALARRIGTDC 479

Db 420 TQASCEBEGYILDDGFICTDIDECENGFCSCGVCHNPGTFECICGPDALARRIGTDC 479

Qy 480 DSGKYDGDSDSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 480 DSGKYDGDSDSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Qy 540 KKQGAARAKMEYKCAAPSKEVVLQHVRTERTPQRL 574

Db 540 KKQGAARAKMEYKCAAPSKEVVLQHVRTERTPQRL 574

RESULT 4

ADD48168

ID ADD48168 standard; protein; 575 AA.

XX

AC ADD48168;

XX

DT 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP_000352, SEQ ID NO 1386C.

XX

KM Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

KM spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

OS Unidentified.

XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI: 2003-268312/26.
XX
XX GENBANK; NP_000352.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Example 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 575 AA;
SQ

Query Match 99.2%; Score 3176.5; DB 7; Length 575;
Best Local Similarity 99.5%; Pred. No. 6.1e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MUGVYVLCALALAGCGFPAPAPPOGSGOCVHHDFALYPGATPLANSQICDGRGHLM 60
DB 1 MUGVYVLCALALAGCGFPAPAPPOGSGOCVHHDFALYPGATPLANSQICDGRGHLM 60
QY 1 TVRSSVADVSTSLANGDGVGRRLMTGLQPPCGDPPKRLGPRGFWMTGDNNTSYS 120
DB 61 TVRSSVADVSTSLANGDGVGRRLMTGLQPPCGDPPKRLGPRGFWMTGDNNTSYS 120
QY 121 RWARLDLNGAPLCPGLCVAVSAABATVSEPIWEEQCEVKADGFLCEHFHPATCRPLAV 180
DB 121 RWARLDLNGAPLCPGLCVAVSAABATVSEPIWEEQCEVKADGFLCEHFHPATCRPLAV 180
QY 121 RWARLDLNGAPLCPGLCVAVSAABATVSEPIWEEQCEVKADGFLCEHFHPATCRPLAV 180
DB 121 RWARLDLNGAPLCPGLCVAVSAABATVSEPIWEEQCEVKADGFLCEHFHPATCRPLAV 180
QY 181 EFGAAAVAVSTYGPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVGSHWARBP 240
DB 181 EFGAAAVAVSTYGPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVGSHWARBP 240

QY 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGAAIQADRSCTAS-TQSCNDICERHFCVNP 299
DB 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGAAIQADRSCTAS-TQSCNDICERHFCVNP 300
QY 300 DQGSYSQMCETGYRLAADQRCEDVDCTLEPSPCORCVNTQSGFCHCYPNYDLYDG 359
DB 301 DQGSYSQMCETGYRLAADQRCEDVDCTLEPSPCORCVNTQSGFCHCYPNYDLYDG 360
QY 360 ECVEPVDPCEFRANCEYOQOPINQTSYLCVCAEGAP1PHEBHRQCMFCNQACPADCPN 419
DB 361 ECVEPVDPCEFRANCEYOQOPINQTSYLCVCAEGAP1PHEBHRQCMFCNQACPADCPN 420
QY 420 TQASCECEBGYILDGFICTDIDECENGFGSCVCHNLPGTFECICGPDALAHRTGDC 479
DB 421 TQASCECEBGYILDGFICTDIDECENGFGSCVCHNLPGTFECICGPDALAHRTGDC 480
QY 480 DSGKVDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCVALLALCHLR 539
DB 481 DSGKVDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCVALLALCHLR 540
QY 540 KKGAAARAKMEYKCAAPSKVVLQHVTRTERPRL 574
DB 541 KKGAAARAKMEYKCAAPSKVVLQHVTRTERPRL 575

RESULT 5
ADN04006
ID ADN04006 standard; protein, 575 AA.
AC ADN04006;
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Antipsoriatic protein sequence #198.
DE
XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
KW
XX
XX Homo sapiens.
OS
XX
XX WO2004028479-A2.
PN
XX
XX 08-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030907.
PF
XX
XX 25-SEP-2002; 2002US-0414006P.
PR
XX
XX (GENTECH) GENENTECH INC.
PA
XX
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
PI
XX
XX WPI: 2004-305105/28.
DR
XX
XX N-PSDB; ADN04005.
DR
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
PT
XX
XX Claim 9; SEQ ID NO 400; 30699P; English.
PS
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
XX Sequence 575 AA;
SQ

Query Match 99.2%; Score 3176.5; DB 8; Length 575;
Best Local Similarity 99.5%; Pred. No. 6.1e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVITGALALAGLPAPAPAPPGSSQCVYHDCFPALYPGPATFLNASQICDGLRGLM 60
 DB 1 MLGVITGALALAGLPAPAPAPPGSSQCVYHDCFPALYPGPATFLNASQICDGLRGLM 60
 QY 61 TVRSSVADVITSLIINGDGVGRRLMTGLQIPGCGDPKRLGRLRGFWTGDNNNTSYS 120
 DB 61 TVRSSVADVITSLIINGDGVGRRLMTGLQIPGCGDPKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RWARLDINGAPLCEPLCAVAVSAEATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDINGAPLCEPLCAVAVSAEATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
 DB 181 EPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
 QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFCVNP 300
 QY 300 DPGSYSCMCTGYRLAADQHRCEVDVDDCILEBSPCPCPCVNTQGFECCHCPNYDLVDG 359
 DB 301 DPGSYSCMCTGYRLAADQHRCEVDVDDCILEBSPCPCPCVNTQGFECCHCPNYDLVDG 360
 QY 360 ECVEPVDFCFRANCEYCOQPLNQTSYLVCAGGAPAPIPHEPHRCQMFNCQTACPADCDPN 419
 DB 361 ECVEPVDFCFRANCEYCOQPLNQTSYLVCAGGAPAPIPHEPHRCQMFNCQTACPADCDPN 420
 QY 420 TQASCECEBGITLDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDALARIHIGTDC 479
 DB 421 TQASCECEBGITLDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDALARIHIGTDC 480
 QY 480 DSGKVDGSDSGSGEPPTPGSTLTPPAVGLVHSGILIGISIASLCLVALLALCHLR 539
 DB 481 DSGKVDGSDSGSGEPPTPGSTLTPPAVGLVHSGILIGISIASLCLVALLALCHLR 540
 QY 540 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 574
 DB 541 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 575

RESULT 6
 ADP12616
 ID ADP12616 standard; protein; 575 AA.
 AC ADP12616;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #226.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 XX
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Mohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2625; 1762bp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 CC
 SQ Sequence 575 AA;
 Query Match 99.2%; Score 3176.5; DB 8; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MLGVITGALALAGLPAPAPAPPGSSQCVYHDCFPALYPGPATFLNASQICDGLRGLM 60
 DB 1 MLGVITGALALAGLPAPAPAPPGSSQCVYHDCFPALYPGPATFLNASQICDGLRGLM 60
 QY 61 TVRSSVADVITSLIINGDGVGRRLMTGLQIPGCGDPKRLGRLRGFWTGDNNNTSYS 120
 DB 61 TVRSSVADVITSLIINGDGVGRRLMTGLQIPGCGDPKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RWARLDINGAPLCEPLCAVAVSAEATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDINGAPLCEPLCAVAVSAEATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
 DB 181 EPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
 QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFCVNP 300
 QY 300 DPGSYSCMCTGYRLAADQHRCEVDVDDCILEBSPCPCPCVNTQGFECCHCPNYDLVDG 359
 DB 301 DPGSYSCMCTGYRLAADQHRCEVDVDDCILEBSPCPCPCVNTQGFECCHCPNYDLVDG 360
 QY 360 ECVEPVDFCFRANCEYCOQPLNQTSYLVCAGGAPAPIPHEPHRCQMFNCQTACPADCDPN 419
 DB 361 ECVEPVDFCFRANCEYCOQPLNQTSYLVCAGGAPAPIPHEPHRCQMFNCQTACPADCDPN 420
 QY 420 TQASCECEBGITLDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDALARIHIGTDC 479
 DB 421 TQASCECEBGITLDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDALARIHIGTDC 480
 QY 480 DSGKVDGSDSGSGEPPTPGSTLTPPAVGLVHSGILIGISIASLCLVALLALCHLR 539
 DB 481 DSGKVDGSDSGSGEPPTPGSTLTPPAVGLVHSGILIGISIASLCLVALLALCHLR 540
 QY 540 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 574
 DB 541 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 575

RESULT 7
 ADO28681
 ID ADO28681 standard; protein; 575 AA.
 AC ADO28681;
 XX

XX 12-AUG-2004 (first entry)
DT Human thrombomodulin protein SEQ ID NO:110.
XX
XX
DE high-grade dysplasia; HGD; oesophageal adenocarcinoma;
XX neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KM thrombomodulin; chromosome 20.
XX
OS Homo sapiens.
XX
XX MO200404178-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036260.
XX
XX 13-NOV-2002; 2002US-0425813P.
XX
XX (GETH) GENENTECH INC.
XX
XX Smith V;
XX
XX WPI; 2004-420319/39.
XX
XX N-PSDB; ADO28680.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
XX of the genes.
XX
XX Example 4; SEQ ID NO 110; 256pp; English.
XX
XX The present invention describes a method for detecting high-grade
XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
XX (1) identifying an oesophageal tissue susceptible to oesophageal
XX adenocarcinoma; (2) determining the predispotion of a mammalian tissue
XX to a neo-plastic transformation by detecting HGD in cells of the tissue;
XX and (3) detecting cancer in a patient. The method can be used in
XX detecting HGD and cancer in cells of a mammalian tissue sample. The
XX method and compositions of the present invention can be used in treating
XX and preventing HGD and cancer, and in gene therapy. The present sequence
XX represents human thrombomodulin, which is used in the exemplification of
XX the present invention. The human thrombomodulin gene is located on
XX chromosome 20.
XX
XX Sequence 575 AA;
SQ
Query Match 99.2%; Score 3176.5; DB 8; Length 575;
Best Local Similarity 99.5%; Pred. No. 6.1e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MLGVIVLALALAGLGPAPAPAPPOGSGSCVEHDCFPALYPPGATPLNLSQICDGRGHM 60
DB 1 MLGVIVLALALAGLGPAPAPPOGSGSCVEHDCFPALYPPGATPLNLSQICDGRGHM 60
QY 61 TYRSSVADVISILANGDGVGRRLMIGLQLPPCGDPKRLGPGFQWVTGDNNTSYS 120
DB 61 TYRSSVADVISILANGDGVGRRLMIGLQLPPCGDPKRLGPGFQWVTGDNNTSYS 120
QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOQCEVKADGFLCEBHFPAATCRPLAV 180
DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOQCEVKADGFLCEBHFPAATCRPLAV 180
QY 181 ERGAALAAVSTYGPAPARAGADPQALPVGSSAAVAAPLGLQIMCTAPPAVGVGHAREAP 240
DB 181 ERGAALAAVSTYGPAPARAGADPQALPVGSSAAVAAPLGLQIMCTAPPAVGVGHAREAP 240
QY 241 GAMDSVNGGCEHACNAIPGARPCOCPAGALQADGRSCTAS-TOSCNLDLCEHCVNP 299
DB 241 GAMDSVNGGCEHACNAIPGARPCOCPAGALQADGRSCTASATDSNDLCEHCVNP 300
QY 300 DQPGSYCMCETGYRLADQHRCEVDDCILBSPPCRCVCNTGGGFECHCYPNYDLVDG 359

DB 301 DQPGSYCMCETGYRLADQHRCEVDDCILBSPPCRCVCNTGGGFECHCYPNYDLVDG 360
QY 360 ECVEPVDPCFRANCEYQOCPQLNQTSYLCVCAEGFAP1PHEBHRCOMFCNQTACPADCPN 419
DB 361 ECVEPVDPCFRANCEYQOCPQLNQTSYLCVCAEGFAP1PHEBHRCOMFCNQTACPADCPN 420
QY 420 TQASCEPREGYLLDDGFTCTDIDECENGFCSSGVCNHLPGFTECICGPDALAHIGTDC 479
DB 421 TQASCEPREGYLLDDGFTCTDIDECENGFCSSGVCNHLPGFTECICGPDALAHIGTDC 480
QY 480 DSGKYDGDSDSGSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALHCLR 539
DB 481 DSGKYDGDSDSGSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALHCLR 540
QY 540 KKQGAARAKMEYKCAAPSKVEVLQHVTERTPORL 574
DB 541 KKQGAARAKMEYKCAAPSKVEVLQHVTERTPORL 575
RESULT 8
ADP79506
ID ADP79506 standard; protein; 575 AA.
XX
XX ADP79506;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human thrombomodulin.
DE Human thrombomodulin; gene therapy; vasotrophic; cardiovascular-gen.;
XX Human; thrombomodulin; gene therapy; vasotrophic; cardiovascular-gen.;
KM neurtotrophic.
XX
XX Homo sapiens.
XX
XX MO2004050844-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038125.
XX
XX 02-DEC-2002; 2002US-0430099P.
XX
XX (BIOV-) BIOVEC LLC.
XX
XX SenGall LR, Wong J;
PI
XX
XX WPI; 2004-461114/43.
XX
XX N-PSDB; ADP79507, ADP79508, ADP79510.
XX
XX Treating vascular diseases, e.g. atherosclerotic cardiovascular disease
PT comprises introducing a DNA sequence encoding a thrombomodulin protein or
PT its variant into a segment of a blood vessel using a gutless adenovirus
PT vector.
XX
XX Claim 2; SEQ ID NO 2; 44pp; English.
XX
XX The present sequence is that of human thrombomodulin (TM). The invention
XX relates to the ex vivo and in vivo expression of the TM gene for
XX treatment of vascular diseases. A method for treating a vascular disease
XX in a mammal comprises: infecting a segment of a blood vessel in vitro
XX using a gutless adenoviral vector which comprises a polynucleotide
XX encoding a thrombomodulin (TM) protein ADP79506 or its variant; and
XX grafting the virus-treated blood vessel in the mammal such that the TM
XX protein or its variant is expressed in an amount sufficient to reduce re-
XX occlusion or intimal hyperplasia in the grafted blood vessel. A method
XX for treating a vascular disease involves: evacuating a clot in a blood
XX vessel; isolating a segment of blood vessel around the evacuation site
XX with a balloon catheter; and infecting the segment of blood vessel in
XX vivo using a gutless adenoviral vector comprising a polynucleotide
XX encoding a TM protein or its variant, such that TM or its variant is
XX expressed in an amount sufficient to reduce re-occlusion or intimal
XX hyperplasia in the infected segment of the blood vessel. A further method
XX for treating a vascular disease comprises administering a gutless

CC adenovirus vector into a segment of a blood vessel using a stent, where
 CC the vector is capable of expressing TM or its variant and is released
 CC only at the treatment site. These methods eliminate the need to inject
 CC large quantities of virus into a patient, thereby reducing viral-related
 CC toxicity. The methods are used for coronary artery bypass, for the
 CC treatment of peripheral vascular diseases, and for the maintenance of
 CC vein access in renal dialysis patients.

CC Sequence 575 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGVIVLGLALAGLGPAPAPBPOGSGQCVBHCDFALYPPGATPLNLSQICDGLRGHLM 60
 DB 1 MGVIVLGLALAGLGPAPAPBPOGSGQCVBHCDFALYPPGATPLNLSQICDGLRGHLM 60
 QY 61 TVRSSVADVISLILNGDGVGRRLMTGLQLPFCGDPKRLGRLGFQWVTGDNNTSYS 120
 DB 61 TVRSSVADVISLILNGDGVGRRLMTGLQLPFCGDPKRLGRLGFQWVTGDNNTSYS 120
 QY 121 RMARLDLNGALPCGFLCVAVSAABATVPSBPIWEBOQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RMARLDLNGALPCGFLCVAVSAABATVPSBPIWEBOQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 BPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPVGLQLMCTAPPGAOGHAREAP 240
 DB 181 BPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPVGLQLMCTAPPGAOGHAREAP 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 QY 300 DOPGSGCMCEGTGRLADQHRCEVDVDCILEPSPCPORCVNTQGGFCHCYPNYDLYDG 359
 DB 301 DOPGSGCMCEGTGRLADQHRCEVDVDCILEPSPCPORCVNTQGGFCHCYPNYDLYDG 360
 QY 360 ECVBVDPCFRANCERYCOPLNQTSYLCVCAEGFAPPIHBBHRCOMFCNQTCAPADCPN 419
 DB 361 ECVBVDPCFRANCERYCOPLNQTSYLCVCAEGFAPPIHBBHRCOMFCNQTCAPADCPN 420
 QY 420 TQASCECEGYILDDGFLCTDIDECENGFGCSGVCHNLPGTEFCICGPDALARRHIGTDC 479
 DB 421 TQASCECEGYILDDGFLCTDIDECENGFGCSGVCHNLPGTEFCICGPDALARRHIGTDC 480
 QY 480 DSGKVDGSDSGSGBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 DB 481 DSGKVDGSDSGSGBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
 QY 540 KKQGAARAKMEYKCAAPSKVVLQHVRTERTPQRL 574
 DB 541 KKQGAARAKMEYKCAAPSKVVLQHVRTERTPQRL 575

RESULT 9

ADR32191 ADR32191 standard; protein; 575 AA.

AC ADR32191;

DT 02-DEC-2004 (first entry)

DE Human thrombomodulin SEQ ID NO:2.

XX chrombotic disease; thrombomodulin; antiarteriosclerotic; pulmonary;

XX hypotensive; antiinflammatory; nephrotropic; nootropic; neuroprotective;

XX gene therapy; atherosclerotic cardiovascular disease;

XX pulmonary hypertension; acute inflammatory diseases;

XX end-stage renal failure disease; Alzheimer's disease.

OS Homo sapiens.

XX

EN WO2004076635-A2.

XX 10-SEP-2004.

XX 25-FEB-2004; 2004WO-US005453.

XX 25-FEB-2003; 2003US-0449408P.

XX (BIOV-) BIOVEC BV.

PI Sehgal LR, Wong J, Seth P;

XX WPI; 2004-653402/63.

XX N-PsDB; ADR32192.

PT Treating a thrombotic disease in a mammal comprises administering to the
 PT mammal a pharmaceutical composition comprising a viral vector, e.g. adeno
 PT -associated virus, retrovirus, or lentivirus.

PS Claim 1; SEQ ID NO 2; 55pp; English.

CC The invention relates to a novel method for treating a thrombotic disease
 CC in a mammal, comprising administering to the mammal a pharmaceutical
 CC composition comprising a viral vector comprising a nucleotide sequence
 CC encoding human thrombomodulin or its variant. The vector is an
 CC adenovirus, preferably a gutless adenovirus. A composition of the
 CC invention has antiarteriosclerotic, pulmonary-gen, hypotensive,
 CC antiinflammatory, nephrotropic, nootropic, and neuroprotective activity,
 CC and may have a use in gene therapy. The methods and compositions are
 CC useful for treating thrombotic disease, such as atherosclerotic
 CC cardiovascular disease, pulmonary hypertension, acute inflammatory
 CC diseases, end-stage renal failure disease, or Alzheimer's disease. The
 CC present sequence represents human thrombomodulin.

XX Sequence 575 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGVIVLGLALAGLGPAPAPBPOGSGQCVBHCDFALYPPGATPLNLSQICDGLRGHLM 60
 DB 1 MGVIVLGLALAGLGPAPAPBPOGSGQCVBHCDFALYPPGATPLNLSQICDGLRGHLM 60
 QY 61 TVRSSVADVISLILNGDGVGRRLMTGLQLPFCGDPKRLGRLGFQWVTGDNNTSYS 120
 DB 61 TVRSSVADVISLILNGDGVGRRLMTGLQLPFCGDPKRLGRLGFQWVTGDNNTSYS 120
 QY 121 RMARLDLNGALPCGFLCVAVSAABATVPSBPIWEBOQCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RMARLDLNGALPCGFLCVAVSAABATVPSBPIWEBOQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 BPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPVGLQLMCTAPPGAOGHAREAP 240
 DB 181 BPGAAAASVITTYGTPFARAGADFOALPVGSSAAVAPVGLQLMCTAPPGAOGHAREAP 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 300
 QY 300 DOPGSGCMCEGTGRLADQHRCEVDVDCILEPSPCPORCVNTQGGFCHCYPNYDLYDG 359
 DB 301 DOPGSGCMCEGTGRLADQHRCEVDVDCILEPSPCPORCVNTQGGFCHCYPNYDLYDG 360
 QY 360 ECVBVDPCFRANCERYCOPLNQTSYLCVCAEGFAPPIHBBHRCOMFCNQTCAPADCPN 419
 DB 361 ECVBVDPCFRANCERYCOPLNQTSYLCVCAEGFAPPIHBBHRCOMFCNQTCAPADCPN 420
 QY 420 TQASCECEGYILDDGFLCTDIDECENGFGCSGVCHNLPGTEFCICGPDALARRHIGTDC 479
 DB 421 TQASCECEGYILDDGFLCTDIDECENGFGCSGVCHNLPGTEFCICGPDALARRHIGTDC 480
 QY 480 DSGKVDGSDSGSGBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 481 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 540
 QY 540 KKGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 Db 541 KKGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 10

ADU06321 standard; protein; 575 AA.

ADU06321;

27-JAN-2005 (first entry)

Novel bronchial cancer-associated human protein SeqID545.

bronchial cancer; cytostatic; tumour-associated protein;

cancer detection; metastasis; tumour; human.

Homo sapiens.

DE10316701-A1.

04-NOV-2004.

09-APR-2003; 2003DE-01016701.

09-APR-2003; 2003DE-01016701.

(HINZ/) HINZMANN B.

(HERM/) HERMANN K.

(CAST/) HEIDEN CASTANOS-VELEZ E.

Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kimmann H;

Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;

WPI; 2004-786403/78.

N-PSDB; ADU05634.

Claim 2; SEQ ID NO 545; 1381bp; German.

This invention relates to a novel isolated nucleic acid associated with

bronchial cancer comprising 489 defined sequences given in the

specification. The invention may be useful for the production of

compounds with a cytostatic activity through the inhibition of expression

or activity of tumour-associated proteins. The novel DNA sequences and

the proteins/peptides encoded by them are used for detecting bronchial

cancer or determining the risk of developing it and to screen for

specific binding partners of the DNA or protein sequences, where the

binding partners are potentially useful as agents for treating or

diagnosing bronchial cancer. The DNA or protein sequences can also be

used for prognosis, detection of metastases and for secondary treatment

(of tumours that have been stabilised or are no longer detectable).

Detecting abnormal expression of the DNA sequences provides early

diagnosis of bronchial cancers. The present sequence is that of a protein

encoded by a novel bronchial cancer-associated human gene sequence of the

invention.

Sequence 575 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 575;

Best Local Similarity 99.5%; Pred. No. 6.1e-175;

Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1 MGVGVVGLALALAGAGFPAPAPBPQSGSCVHDCFPALYPGPATPLNLSQICDGRHLM 60

1 MGVGVVGLALALAGAGFPAPAPBPQSGSCVHDCFPALYPGPATPLNLSQICDGRHLM 60

QY 61 TVRSSVAADVITSLINDGCVGRRRLNIQLQLPFGCCDPKRLGRLRGQWYTGNNNTSYS 120
 Db 61 TVRSSVAADVITSLINDGCVGRRRLNIQLQLPFGCCDPKRLGRLRGQWYTGNNNTSYS 120
 QY 121 RMARLDLNGAPLCGPLCAVAASAATVPSBPITWEEQCEVADGFLCEFHFPATCRPLAV 180
 Db 121 RMARLDLNGAPLCGPLCAVAASAATVPSBPITWEEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 Db 181 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 QY 241 GAMDCSVNCGCEHACNAIPAPRCQCPAGALQADGSCFASATQSCNDLCEHFCVNP 299
 Db 241 GAMDCSVNCGCEHACNAIPAPRCQCPAGALQADGSCFASATQSCNDLCEHFCVNP 300
 QY 300 DQPSYSCMCEYTRLAADHRCEDVDDCIIEPSPCPCPCVNTQGGFECCHCYPNVDLVG 359
 Db 301 DQPSYSCMCEYTRLAADHRCEDVDDCIIEPSPCPCPCVNTQGGFECCHCYPNVDLVG 360
 QY 360 ECVBPVPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTACPADCPN 419
 Db 361 ECVBPVPCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTACPADCPN 420
 QY 420 TQASCECPBGYITLDGFTCTIDECENGFCSCGYCHNLPTFECTICGPDLSLAHHIGTDC 479
 Db 421 TQASCECPBGYITLDGFTCTIDECENGFCSCGYCHNLPTFECTICGPDLSLAHHIGTDC 480
 QY 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 539
 Db 481 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 540
 QY 540 KKGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 Db 541 KKGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 11

ABG72572 standard; protein; 631 AA.

ABG72572;

05-MAR-2003 (first entry)

Human thrombomodulin protein #1 (CD141).

Human; thrombomodulin; CD141; dendritic cell separation; inflammation;

antiinflammatory; cytostatic; antiarthritic; antineumatic;

immunopressive; dermatological; cell therapy; dermatomyositis; cancer;

autoimmune disorder; rheumatoid arthritis; psoriatic arthritis;

alkylosing spondylitis; Sjorgen's syndrome; lupus erythematosus;

Goodpasture's syndrome; scleroderma; vasculitis; polyomyositis.

Homo sapiens.

WO200293172-A1.

21-NOV-2002.

17-MAY-2002; 2002WO-US015786.

17-MAY-2001; 2001US-0291561P.

(MILT-) MILTENYI BIOTEC INC.

Schmitz J, Dzionek A, Buck DW;

WPI; 2003-129324/12.

Enriching for dendritic cells from a mixture of cells, useful for

treating inflammation, cancer or autoimmune disorders such as arthritis,

or lupus by contacting the mixture of cell with an antigen-binding

PT fragment specific for CD141.

XX PS Example 1; Fig 3A; 88pp; English.

XX CC This invention relates to a novel method for separating dendritic cells
CC from a mixture of cells. The method comprises contacting the mixture of
CC cells with an antigen-binding fragment specific for CD141, and selecting
CC the cells that are CD141 positive therefore producing a dendritic cell-
CC enriched composition. The method of the invention may have
CC antiinflammatory, cytostatic, antiarthritic, antineumatic,
CC immunosuppressive and dermatological activities and may be used in cell
CC therapy. The methods, compositions and agents of the invention are useful
CC for treating inflammation, cancer or autoimmune disorders such as
CC rheumatoid arthritis, psoriatic arthritis, alkylosing spondylitis,
CC Sjogren's syndrome, lupus erythematosus, Goodpasture's syndrome,
CC scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic
CC cells and populations are useful for screening assays for agents that
CC affect dendritic cell function, and for the phenotypic, functional,
CC biochemical or molecular analyses of dendritic cells. The compositions
CC and dendritic cells are useful as vaccine adjuvants. The present sequence
CC represents a protein sequence of human CD141 protein which is used to
CC generate the dendritic cell specific antibodies that are used in the
CC method of the invention

XX SQ Sequence 631 AA;

Query Match 99.2%; Score 3176.5; DB 6; Length 631;

Best Local Similarity 99.5%; Pred. No. 6.7e-175; Indels 1; Gaps 1;

Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGFPAAPAPQPGSGSQVEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 57 MLGVLVIGALALAGLGFPAAPAPQPGSGSQVEHDCFALYPGPATFLNASQICDGLRGHLM 116
QY 61 TVRSSVADVLSLLNGDGGVGRRLWTGLQLPGCCGPKRLGRLRGFWMTGDNNTSYS 120
DB 117 TVRSSVADVLSLLNGDGGVGRRLWTGLQLPGCCGPKRLGRLRGFWMTGDNNTSYS 176
QY 121 RMARLDLNGALPCGPLCAVAASAATVPSPIWEQCEVADGFLCFHFPATCRPLAV 180
DB 177 RMARLDLNGALPCGPLCAVAASAATVPSPIWEQCEVADGFLCFHFPATCRPLAV 236
QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWRAP 240
DB 237 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWRAP 296
QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCCEHFCVNP 299
DB 297 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCCEHFCVNP 356
QY 300 DQPSYSMCETGYRLADQRCEDVDCTIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 359
DB 357 DQPSYSMCETGYRLADQRCEDVDCTIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 416
QY 360 ECVBPVDFCFRANCEYQCPINQTSYLCVCAEGFAPLIEBPHRCOMFCNQTACPADCDPN 419
DB 417 ECVBPVDFCFRANCEYQCPINQTSYLCVCAEGFAPLIEBPHRCOMFCNQTACPADCDPN 476
QY 420 TQASCECEBYILLDDGFICTDIDCEGNGFCGSGVCHNLPGTFECTCGPSALARRHTGDC 479
DB 477 TQASCECEBYILLDDGFICTDIDCEGNGFCGSGVCHNLPGTFECTCGPSALARRHTGDC 536
QY 480 DSGVVDGSDSGSGBPPSPPTGSLTTPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB 537 DSGVVDGSDSGSGBPPSPPTGSLTTPAVGLVHSGLLIGISIASLCLVALLALLCHLR 596
QY 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTRTERTPQRL 574
DB 597 KKQGAARAKMEYKCAAPSEKVVLLQHVTRTERTPQRL 631

RESULT 12
ADN05602

ID ADN05602 standard; protein; 681 AA.

XX AC ADN05602;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic protein sequence #966.

XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

PN WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GETH) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

P1 Wu TD;

DR WPI; 2004-305105/28.

DR N-PSDB; ADN05601.

PT New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.

PS Claim 9; SEQ ID NO 1996; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

XX treating psoriasis or a sequence having at least 80% identity to the

XX above sequences. The nucleic acid is useful for preparing a composition

XX for diagnosing or treating psoriasis in a mammal. This sequence

XX corresponds to one of the polypeptides of the invention.

XX SQ Sequence 681 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 681;

Best Local Similarity 99.5%; Pred. No. 7.2e-175; Indels 1; Gaps 1;

Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGFPAAPAPQPGSGSQVEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 107 MLGVLVIGALALAGLGFPAAPAPQPGSGSQVEHDCFALYPGPATFLNASQICDGLRGHLM 166
QY 61 TVRSSVADVLSLLNGDGGVGRRLWTGLQLPGCCGPKRLGRLRGFWMTGDNNTSYS 120
DB 167 TVRSSVADVLSLLNGDGGVGRRLWTGLQLPGCCGPKRLGRLRGFWMTGDNNTSYS 226
QY 121 RMARLDLNGALPCGPLCAVAASAATVPSPIWEQCEVADGFLCFHFPATCRPLAV 180
DB 227 RMARLDLNGALPCGPLCAVAASAATVPSPIWEQCEVADGFLCFHFPATCRPLAV 286
QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCCEHFCVNP 299
DB 287 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWRAP 346
QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCCEHFCVNP 299
DB 287 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWRAP 346
QY 347 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCCEHFCVNP 406
DB 347 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCCEHFCVNP 406
QY 300 DQPSYSMCETGYRLADQRCEDVDCTIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 359
DB 407 DQPSYSMCETGYRLADQRCEDVDCTIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 466
QY 360 ECVBPVDFCFRANCEYQCPINQTSYLCVCAEGFAPLIEBPHRCOMFCNQTACPADCDPN 419
DB 467 ECVBPVDFCFRANCEYQCPINQTSYLCVCAEGFAPLIEBPHRCOMFCNQTACPADCDPN 526

XX Novel polypeptide obtd. by culturing transformed fungus - having blood
 PT coagulation preventing, platelet aggregation preventing and thrombolytic
 PT activities.
 XX
 XX Disclosure; Fig 55; 65pp; Japanese.
 XX
 CC Novel polypeptides, obtd. by culturing transformed fungus, have blood
 CC coagulation preventing, platelet aggregation preventing and thrombolytic
 CC activities. In an example, plasmid M3impl19TM23 (constructed from pSV2TM2
 CC (ATCC 67228) contg. a human thrombomodulin sequence) was subjected to
 CC site directed mutagenesis to prepare pSV2TM27. Plasmid pSV2TM27 was
 CC transfected to COS-1 cells. The activity of promoting protein C
 CC activation by thrombin of the peptide produced by the transformed COS-1
 CC cell was measured. The amt. of the peptide was determined
 CC
 XX Sequence 575 AA;
 SQ
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1e-174;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MLGVIVLGLALAGLGFAPAPAPPOGSGQCVBHDGFALYPPATFLNASQICDGLRGHLM 60
 DB 1 MLGVIVLGLALAGLGFAPAPAPPOGSGQCVBHDGFALYPPATFLNASQICDGLRGHLM 60
 QY 61 TVRSSVADVLSILNLDGSGVGRRLMTGLQLPFGCGDKRLGRLGFGQWMTGDNNTSYS 120
 DB 61 TVRSSVADVLSILNLDGSGVGRRLMTGLQLPFGCGDKRLGRLGFGQWMTGDNNTSYS 120
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAIVSTTGGPPARAGADFOALPVGSSAAVAPLGLQMLCTAPGAVOGHARBAR 240
 DB 181 EPGAAAIVSTTGGPPARAGADFOALPVGSSAAVAPLGLQMLCTAPGAVOGHARBAR 240
 QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCSTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCSTAS-TQSCNDLCEHFCVNP 299
 QY 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILBSPCPORCVNTQGFCHCYPNYDLVDG 359
 DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILBSPCPORCVNTQGFCHCYPNYDLVDG 359
 QY 360 ECVBVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 DB 360 ECVBVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 QY 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHTDNC 479
 DB 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHTDNC 479
 QY 480 DSGKVDGSDSGSBPPTPGSTLTTPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 DB 480 DSGKVDGSDSGSBPPTPGSTLTTPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 QY 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 574
 DB 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 574
 RESULT 15
 AAR43031
 ID AAR43031 standard; protein; 575 AA.
 XX
 AC AAR43031;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX
 DE Human thrombomodulin.

XX Anticoagulant; platelet aggregation inhibitor; protein C; activation;
 KW thrombin; thrombomodulin; coagulation disorder; thrombosis;
 KW myocardial infarction; embolism; telangiectasis;
 KW arteriosclerosis obliterans; disseminated intravascular coagulation; DIC;
 KW angina pectoris; gestosis; transient ischaemic attack.
 XX
 XX Homo sapiens.
 XX
 PN WO9322447-A1.
 XX
 PD 11-NOV-1993.
 XX
 PF 30-APR-1993; 93WO-JP000578.
 XX
 PR 01-MAY-1992; 92JP-00112903.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Zushi M, Kondo S, Toma K;
 XX
 DR WPI; 1993-368806/46.
 XX
 PT Peptide with anticoagulant and platelet aggregation inhibitor activity -
 PT which promotes protein C activation by thrombin and is useful in treating
 PT coagulation disorders e.g. thrombosis.
 XX
 PS Disclosure; Fig 1; 84pp; Japanese.
 XX
 CC New peptides (see AAR50069) are inhibitors of the blood coagulation and
 CC platelet aggregation activities of thrombin and promote the protein-C
 CC activation effect of thrombin. They can be produced efficiently in pure
 CC form by culture of appropriate transformants, and are useful in treatment
 CC of circulatory disorders such as myocardial infarction, thrombosis,
 CC embolism, telangiectasis, arteriosclerosis obliterans, disseminated
 CC intravascular coagulation, angina pectoris, gestosis and transient
 CC ischaemic attack. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 575 AA;
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1e-174;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MLGVIVLGLALAGLGFAPAPAPPOGSGQCVBHDGFALYPPATFLNASQICDGLRGHLM 60
 DB 1 MLGVIVLGLALAGLGFAPAPAPPOGSGQCVBHDGFALYPPATFLNASQICDGLRGHLM 60
 QY 61 TVRSSVADVLSILNLDGSGVGRRLMTGLQLPFGCGDKRLGRLGFGQWMTGDNNTSYS 120
 DB 61 TVRSSVADVLSILNLDGSGVGRRLMTGLQLPFGCGDKRLGRLGFGQWMTGDNNTSYS 120
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAIVSTTGGPPARAGADFOALPVGSSAAVAPLGLQMLCTAPGAVOGHARBAR 240
 DB 181 EPGAAAIVSTTGGPPARAGADFOALPVGSSAAVAPLGLQMLCTAPGAVOGHARBAR 240
 QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCSTAS-TQSCNDLCEHFCVNP 299
 DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCSTAS-TQSCNDLCEHFCVNP 299
 QY 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILBSPCPORCVNTQGFCHCYPNYDLVDG 359
 DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILBSPCPORCVNTQGFCHCYPNYDLVDG 359
 QY 360 ECVBVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 DB 360 ECVBVDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 QY 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHTDNC 479
 DB 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHTDNC 479

Db	421	TOASCCEPBEYI LDDGFICTDIDECENGFCSGVCHNLPGTFECICGPD SALTVRHIGTDC	480
Qy	480	DSGKVDGDDSGSGRPPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVVALLALCHLR	539
Db	481	DSGKVDGDDSGSGRPPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVVALLALCHLR	540
Qy	540	KKOGARAKMEYKCAAPSKEVVLQHVRTERTPORL	574
Db	541	KKOGARAKMEYKCAAPSKEVVLQHVRTERTPORL	575

Search completed: February 4, 2006, 04:27:57
 Job time : 202 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 4, 2006, 04:28:12 ; Search time 45 Seconds
(without alignments)
1227.298 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MGVYLVGALAGLGGFPAP.....APSKVVLQHVRTTPTQL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3172.5	99.0	575	1 THHUB	thrombomodulin pre
2	2113.5	66.0	577	2 A6501	thrombomodulin pre
3	1314	41.0	356	2 A25918	thrombomodulin - b
4	414.5	12.9	1574	2 T13954	MEGF6 protein - ra
5	411	12.8	1620	2 T27283	hypothetical prote
6	384	12.0	2871	2 A55567	fibrillin I - bovi
7	384	12.0	3002	2 A47221	fibrillin I precu
8	382	11.9	2871	2 A55624	fibrillin-1 precu
9	374.5	11.7	2907	2 A57278	fibrillin-2 precu
10	373.5	11.7	2918	2 A54105	fibrillin-2 precu
11	363	11.3	1184	2 A55184	fibrillin-2 precu
12	358.5	11.2	741	2 T46488	hypothetical prote
13	356.5	11.1	1221	2 A49457	fibrillin-2 precu
14	333	10.4	1712	2 A38261	masking protein pr
15	330.5	10.3	589	2 T43210	fibrillin-1D precu
16	325	10.1	1394	2 A35626	transforming growt
17	324	10.1	689	2 T42760	fibrulin, splice fo
18	324	10.1	712	2 T42990	fibrulin 1, splice
19	323.5	10.1	1964	2 T09059	notch3 - mouse
20	315.5	9.9	2321	2 S78549	notch3 protein - h
21	312.5	9.8	798	2 T27793	hypothetical prote
22	310.5	9.7	601	2 B36346	fibrulin 1 precu
23	310.5	9.7	683	2 C36346	fibrulin 1 precu
24	308	9.6	1820	2 A55494	latent transformin
25	304	9.5	3507	2 T34513	hypothetical prote
26	303.5	9.5	685	2 S78040	fibrulin, splice fo
27	302.5	9.4	705	2 S34968	fibrulin, splice fo
28	300	9.4	1251	2 A57293	latent transformin
29	288	9.0	2437	2 S42612	transmembrane prot

30	286.5	8.9	2531	2 A46019	notch-1 protein -
31	285.5	8.9	2352	2 T30201	Notch homolog prot
32	284.5	8.9	2471	2 A49128	cell-fate determin
33	284	8.9	2703	1 A24420	notch protein - fr
34	283.5	8.9	2318	2 S45306	notch 3 protein -
35	281	8.8	387	2 I38449	extracellular prot
36	277.5	8.7	511	2 T17298	hypothetical prote
37	275	8.6	493	2 JC5621	epidermal growth f
38	273.5	8.5	2531	2 S18188	notch protein homo
39	270	8.4	2555	2 A40043	notch protein homo
40	263.5	8.2	1203	2 A49175	Notch B protein -
41	263.5	8.2	1217	1 EGM5WG	epidermal growth f
42	263	8.2	2531	2 T31070	notch homolog - se
43	257	8.0	2524	2 A35844	Xotch protein - Af
44	254	7.9	674	2 I55476	growth potentiatio
45	253.5	7.9	1133	1 EGRT	epidermal growth f

ALIGNMENTS

RESULT 1

THHUB
thrombomodulin precursor [validated] - human
C.Species: Homo sapiens (man)
C.Date: 31-Dec-1988 #sequence revision 12-May-1995 #text change 09-Jul-2004
C.Accession: A41442; A28307; A29680; A27073; JX0264; S38954
R.Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama
J. Biochem. 103, 281-285, 1988
A.Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activ
A.Reference number: A41442; MUID:88227901; PMID:283377
A.Accession: A41442
A.Molecule type: DNA
A.Residues: 1-575 <SHI>
A.Cross-references: UNIPROT:P07204; UNIPARC:UPI00000498FB; DDBJ:D00210; NID:g220126; PID
R.Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenbery, R.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
A.Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
A.Reference number: A28307; MUID:87317665; PMID:2819876
A.Accession: A28307
A.Molecule type: DNA; mRNA
A.Residues: 1-472, 'A', 474-575 <JAC>
A.Cross-references: UNIPARC:UPI0000002BD; GB:J02973; NID:g339658; PIDN:AA61175.1; PID
R.Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioke, J.; Maruyama, I.; Zushi, M.; Kawana
EMBO J. 6, 1891-1897, 1987
A.Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
A.Reference number: A29680; MUID:88004395; PMID:2820710
A.Accession: A29680
A.Molecule type: mRNA
A.Residues: 1-575 <SUZ>
A.Cross-references: UNIPARC:UPI00000498FB; GB:X05495; NID:g37123; PIDN:CAA29045.1; PID:g
A.Experimental source: lung endothelium
A.Note: part of this sequence, including the amino end of the mature protein, were deter
R.Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
Biochemistry 26, 4350-4357, 1987
A.Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
A.Reference number: A27073; MUID:88024950; PMID:2822087
A.Accession: A27073
A.Molecule type: mRNA
A.Residues: 1-472, 'A', 474-575 <WEN>
A.Cross-references: UNIPARC:UPI0000002BD; GB:M16552; NID:g339656; PIDN:AAB5908.1; PID
A.Experimental source: placenta
A.Note: parts of this sequence were determined by protein sequencing
R.Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
J. Biochem. 113, 433-440, 1993
A.Title: Urinary thrombomodulin, its isolation and characterization.
A.Reference number: JX0264; MUID:93293792; PMID:8390446
A.Accession: JX0264
A.Molecule type: protein; mRNA
A.Residues: 19-472, 'A', 474-486 <YAM>
A.Cross-references: UNIPARC:UPI000017341
A.Experimental source: urine
A.Note: the urinary form appears to be identical with that circulating in plasma

R;Gerlitz, B.; Haessell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
Biochem. J. 295, 131-140, 1993
A:Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
serine.
A:Reference number: S38954; MUID:94029900; PMID:8216207
A:Accession: S38954
A:Molecule type: protein
A:Residues: 475-491, 'X', 493-494 <GER>
A:Cross-references: UNIPARC:UPI0000173342
A:Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
R;Meininger, D.P.; Komives, E.A.
submitted to the Brookhaven Protein Data Bank, September 1995
A:Reference number: A67369; PDB:1L2Q
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, August 1994
A:Reference number: A52804; PDB:1HLT
A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
R;Hrabal, R.; Komives, E.A.; Ni, F.
submitted to the Brookhaven Protein Data Bank, November 1995
A:Reference number: A65583; PDB:1FGD
A:Contents: annotation; conformation by (1)H-NMR, residues 427-444
R;Hrabal, R.; Komives, E.A.; Ni, F.
Protein Sci. 5, 195-203, 1996
A:Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the
A:Reference number: A58595; MUID:96276211; PMID:8745396
A:Contents: annotation; conformation by (1)H-NMR
C:Genetics:
A:Gene: GDB:THBD
A:Cross-references: GDB:119613; OMIM:188040
A:Map position: 20p11.2-20p11.2
A:introns: #status absent
C:Complex: homodimer, urinary form
C:Function:
A:Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
A:Pathway: blood coagulation moderation
A:Note: the membrane-bound form is located on the endothelium luminal surface of arterie
A:Note: thrombin complexed with the membrane-bound form is subject to endocytosis
C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
C:Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coag
e protein
F:1-18/Domain: signal sequence #status predicted <STG>
F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
F:19-513/Domain: extracellular #status predicted <EXT>
F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
F:24-167/Domain: C-type lectin homology <LCH>
F:177-199/Region: PEST sequence
F:201-233/Region: PEST sequence
F:245-280/Domain: EGF homology <EG1>
F:288-323/Domain: EGF homology <EG2>
F:329-362/Domain: EGF homology <EG3>
F:369-404/Domain: EGF homology <EG4>
F:408-439/Domain: EGF homology <EG5>
F:445-480/Domain: EGF homology <EG6>
F:485-513/Region: PEST sequence
F:517-539/Domain: transmembrane #status predicted <TMN>
F:540-575/Domain: intracellular #status predicted <INT>
F:47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:174,228,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374-38
F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:324/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F:490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimen

Query Match 99.0%; Score 3172.5; DB 1; Length 575;
Best Local Similarity 99.3%; Pred. No. 7.3e-182;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVVLTALAGLGPAPAPPOGGSCVHHDPALYPPGATFLNAGQICDGLRGHLM 60
DB 1 MGVVLTALAGLGPAPAPPOGGSCVHHDPALYPPGATFLNAGQICDGLRGHLM 60
QY 61 TVRSSVADVLSILNDGSGVRRRLMIGLQLPPGCGDKRLGFLRGFWTGDNNISYS 120

DB 61 TVRSSVADVLSILNDGSGVRRRLMIGLQLPPGCGDKRLGFLRGFWTGDNNISYS 120
QY 121 RMARLDLNGADLCGPLCAVAASAATVSEPIWEEOQCEVADGFLCEHFPATCRPLAV 180
DB 121 RMARLDLNGADLCGPLCAVAASAATVSEPIWEEOQCEVADGFLCEHFPATCRPLAV 180
QY 181 EPGAAAAAVSTTGTTPPARADFOALPVGSSAAVAPLGLDMCTAPPGAVQGHMAREAP 240
DB 181 EPGAAAAAVSTTGTTPPARADFOALPVGSSAAVAPLGLDMCTAPPGAVQGHMAREAP 240
QY 241 GAMDCSVNCGCEHACNAIPGAPPCQCPAGAAADGSCFAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVNCGCEHACNAIPGAPPCQCPAGAAADGSCFAS-TQSCNDLCEHFCVNP 300
QY 300 DQPGSGSCMCEGTGYRLADQHRCEVDVDCILEPSPCPCVNTQGFECCHCYPNYDLVDG 359
DB 301 DQPGSGSCMCEGTGYRLADQHRCEVDVDCILEPSPCPCVNTQGFECCHCYPNYDLVDG 360
QY 360 ECVFVDPDCEFRANCEYQCPLNQTSTYLCVCAEGFAPPIHEBHRQMFNCQTAAPADCDPN 419
DB 361 ECVFVDPDCEFRANCEYQCPLNQTSTYLCVCAEGFAPPIHEBHRQMFNCQTAAPADCDPN 420
QY 420 TQASCEGEGYILDDGFLCTDIDECENGFCSCVCHNLPTFECCICGPDALARIHIGTDC 479
DB 421 TQASCEGEGYILDDGFLCTDIDECENGFCSCVCHNLPTFECCICGPDALARIHIGTDC 480
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCIVALLAILCHLR 539
DB 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCIVALLAILCHLR 540
QY 540 KKQGAARAKMEYKCAAPSEKVVLLQHVRETRPQRL 574
DB 541 KKQGAARAKMEYKCAAPSEKVVLLQHVRETRPQRL 575

RESULT 2
A60501
thrombomodulin precursor - mouse
N:Alternate names: fetomodulin
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S08488; A32001; A60501
R:Dicman, W.A.; Majerus, P.W.
Nucleic Acids Res. 17, 802, 1989
A:Title: Sequence of a cDNA for mouse thrombomodulin and comparison of the predicted mou
A:Reference number: S08488; MUID:89128454; PMID:2536925
A:Accession: S08488
A:Molecule type: mRNA
A:Residues: 1-577 <DIR>
A:Cross-references: UNIPROT:P15306; UNIPARC:UPI00000197C; EMBL:X14432; NID:954781; PIDN
R:Dicman, W.A.; Kumada, T.; Sadler, J.E.; Majerus, P.W.
J. Biol. Chem. 263, 15815-15822, 1988
A:Title: The structure and function of mouse thrombomodulin. Phorbol myristate acetate s
A:Reference number: A32001; MUID:89008498; PMID:2844823
A:Accession: A32001
A:Molecule type: mRNA
A:Residues: 97-577 <DIR>
A:Cross-references: UNIPARC:UPI0000176503; GB:J04060
R:Imada, S.; Yamaguchi, H.; Nagumo, M.; Katsuyangsi, S.; Iwasaki, H.; Imada, M.
Dev. Biol. 140, 113-122, 1990
A:Title: Identification of fetomodulin, a surface marker protein of fetal development, a
A:Reference number: A60501; MUID:90292331; PMID:2162790
A:Accession: A60501
A:Molecule type: protein
A:Residues: 19-22,330-343,479-489,545-555,562-575 <IMA>
A:Cross-references: UNIPARC:UPI00001746F0; UNIPARC:UPI0000176504; UNIPARC:UPI0000176505;
C:Comment: Thrombomodulin binds to and internalizes with thrombin. It is also a cofactor
C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
C:Keywords: anticoagulant; membrane protein; phosphoprotein; receptor
F:24-165/Domain: C-type lectin homology <LCH>
F:244-279/Domain: EGF homology <EG1>
F:287-322/Domain: EGF homology <EG2>

F:328-361/Domain: EGF homology <EG3>
 F:368-403/Domain: EGF homology <EG4>
 F:407-438/Domain: EGF homology <EG5>
 F:444-479/Domain: EGF homology <EG6>

Query Match 66.0%; Score 2113.5; DB 2; Length 577;
 Best Local Similarity 67.0%; Pred. No. 8.3e-119;
 Matches 388; Conservative 53; Mismatches 129; Indels 9; Gaps 5;

QY 1 MLGVVLALALAGFPAPAPAPGSGCVCVHDFCALPYGPATLNAISQICDGRGHL 60
 DB 1 MLGIFFLVLPASIGLSALALQPTGSCVHBCFALFQGPATLDSQACQRLQGHLM 60
 QY 61 TVRSSVADVLSLLINGDG-GVGRRLWIGLQPPGCGPKRIGPLRGFWYTGDNNTSY 119
 DB 61 TVRSSVADVLSLLSQQSMIDGP---WIGLQPPGCGDDPHLGLRFGWYTGDNNTSY 117
 QY 120 SRMARLDLNGAPLCPGLCVAVSAAEATVPSEPIWEEQCEVADFLCEFPHPATCRPLA 179
 DB 118 SRMARPNDOATPLCPGLCVAVSTATAEAGBEPAMEKECEETQGLCEFYFTASCRLPLT 177
 QY 180 VEP-GAAAASITVGFEPFARGADFOALPVGSSAAVPLGLQIMCTAPRGAVQGMARE 238
 DB 178 VNTDPEAAHISTNTTFVGSADFOPLPVGSSAAVEPLGLEIVCARPFGTSBGHAME 237
 QY 239 APGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVP 297
 DB 238 ATGAMNCSVENGGCEYLNRSTNEPRCLCPRDMDLQADGRCARVVGSCNLECHFCVS 297
 QY 298 NPDPGSGSCMCEGYRLAADQHRCEVDCTLEBSPCPQRCVNTQGGFECPCPNYDLV 357
 DB 298 NAEVPGSGSCMCEGYQLAADGHRCEVDCKQGNPQPCVMTKGGFECGYDGYELV 357
 QY 358 DGECEPDPGCFRANCERQCOPLNQTSTLCVCAEFAPIRHPHRCQMFQCTACRPACD 417
 DB 358 DGECEVLDPCFGSCFQCPVSTDRICAPFAPKPBPHKCEMFQCTSCPADCD 417
 QY 418 PNTQASCECPGYIILDDFICTDIDECENGGFCGVCHNLPGTFEFCIGPSPALARIHT 477
 DB 418 PNTPTVCECPGYIILDBSVCTDIDECQSGCFSTSECNPFQSGYECIGCPPTALAGQISK 477
 QY 478 DCDGSKV---DGDGSGSGEPSPSTLTPPAVLVHSGLLIGISIASLCTVALLAL 534
 DB 478 DCDP1PVREDTKEBEGSEPPSPPTGPTGPPSPARPHSVGLIGISIASLCTVALLAL 537
 QY 535 LCHIRKKGARARMEYKCAAPSKKVTLQHVTERTEPQR 573
 DB 538 LCHIRKKGARARMEYKCAASAKEVYLQHVTRDTLQK 576

RESULT 3

A25918
 thrombomodulin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A25918
 R:Juckman, R.W.; Beeler, D.L.; Vandewater, L.; Rosenberg, R.D.
 A:Title: Characterization of a thrombomodulin cDNA reveals structural similarity to the
 A:Reference number: A25918; MUID:87067408; PMID:3024152
 A:Accession: A25918
 A:Molecule type: mRNA
 A:Residues: 1-356 <JUG>
 A:Cross-references: UNIPROT:P06579; UNIPARC:UPI000013732F; GB:M14657; NID:9163762; PTDN:
 C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: transmembrane protein
 F:21-56/Domain: EGF homology <EG1>
 F:64-97/Domain: EGF homology <EG2>
 F:103-136/Domain: EGF homology <EG3>
 F:143-178/Domain: EGF homology <EG4>
 F:182-213/Domain: EGF homology <EG5>
 F:219-253/Domain: EGF homology <EG6>

Query Match 41.0%; Score 1314; DB 2; Length 356;
 Best Local Similarity 65.0%; Pred. No. 2.2e-71;
 Matches 232; Conservative 42; Mismatches 67; Indels 16; Gaps 7;

QY 229 GAVQHWARREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSC-TASTQSC 287
 DB 5 GETERBWRREAPGAMACVVERGCGCHECKGASAGSNCLCPADALQADGRSGGLPAEHPC 64
 QY 288 NDLCHEFCVPPDDQGSYSCEGYRLAADQHRCEVDCTLEBSPCPQRCVNTQGGPE 347
 DB 65 HOLCEHFC-HHGLGANTTICIEAGYQLAADQHRCEVDCTLEBSPCPQRCVNTQGGPE 122
 QY 348 CHCPYNDLVDBCEPEPDPGCFRANCERQCOPLNQTSTLCVCAEFAPIRHPHRCQMF 407
 DB 123 CHCOTGYLVDBCECPDPDPGCFDNNECYQCPVGRSHKICABEFAVPAPGPHKQMF 182
 QY 408 NOTACPADCDPNTQASCECPGYIILDDFICTDIDECENGGFCGVCHNLPGTFEFCIGP 467
 DB 183 NOTSCPADCDHPYPTICRCPGYIILDBSVCTDINECDT-NICPGCHNLPGTFEFCIGP 241
 QY 468 DSALAHITGTDGSGKV-----DGDGSGSGEPSPSTLTP-PA-VGLVHSGLL 517
 DB 242 DSALSGQIGIDCDPTQVNERGTPEDYG--GSGEPVSPGATAPSPAPAGPLHSGVL 299
 QY 518 IGISIASLCTVALLALCHIRKKGARARMEYKCAAPSKKVTLQHVTERTEPQR 574
 DB 300 VGISIASLCTVALLALCHIRKKGASRGLERKCGVPAREMLVQVKTERTTQKL 356

RESULT 4

T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9639030
 A:Accession: T13954
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:93449293;
 A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF6

Query Match 12.9%; Score 414.5; DB 2; Length 1574;
 Best Local Similarity 34.2%; Pred. No. 2.8e-17;
 Matches 104; Conservative 28; Mismatches 101; Indels 71; Gaps 17;

QY 224 CTAPPG-AVOGHWARREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTA 282
 DB 147 CRCPGYQLQDD-GKTCQVDDECAHNGGCGHRCVNTPGSYLCCKXGFLHTDGRCTLA 205
 QY 283 STQSC---NDLCHEFCVP-----NPDQPGSGSCM----- 308
 DB 206 -ISSCTLGNGCQHQCVQLTVTQHRCCQRPQYQLQEDGRRRCVRSFPAEAGGGMHCQ 264
 QY 309 -----CETGYRLADQHRCEVDCTLEBSPCPQRCVNTQGGFECPCPNYDL-VDG 359
 DB 265 IRLGLAHGCHPGYQLADRKTCEDVDECALGALQAGCAGCINTQGSFKCVCHAGYELGADG 324
 QY 360 -EC---VEPYDPCFRAN--CEYQCPPLNQTSTLCVCAEFAPIRHPHRCQMF----- 407
 DB 325 RQCYRIMEIIVNSCEANGGCSHCSH-TSTGPLCTCPRGY-----ELDEQKTCIDIDD 378
 QY 408 --NOTACPADCDPNTQAC--SCEGEGYIIL-DGFTCIDIDECENG-GFCGVCCHNLGTF 461
 DB 379 CAISPCCQAC-ANTPGYECSCFAPGYRLNTDGGCGCDVBCASGHGCGCHEHCSNLGSP 437
 QY 462 ECIC 465

Db 438 QCFC 441

RESULT 5

T27283 hypothetical protein Y64G10A.f - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27283

R/Accession: R submitted to the EMBL Data Library, September 1999

A/Reference number: Z20336

A/Accession: T27283

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1620 <Y64G10A.f>

A/Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAM54471.1;

A/Experimental source: clone Y64G10A

A/Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 12.8%; Score 411; DB 2; Length 1620; Best Local Similarity 25.9%; Pred. No. 4, 6e-17; Matches 142; Conservative 47; Mismatches 197; Indels 162; Gaps 25;

119 YSRMARLNLNGAPLCGPLCVANVSAE-----ATVSPPIWEQOC--YKADFLTEF 169

Db 56 YLRFRFRFRRCGSKCCLRVQANGADLCHNGCTVPSBHNDNEGVCECPVFTAKQY 115

QY 170 HFPATCRPLAVEPGAAAAAVSTVGTTPAARGADFOALPVSSAAVAPLGLQMLTAPRG 229

Db 116 D-ANEC--MANNGGCEHCVN-TIGTY-----CRCWPG 145

QY 220 AVQGMAREARAWMCSEVNGGCEHCNCAIIGARPCQCPAGALADGRSCTASTQSC-- 287

Db 146 FELSGDNGTCSDDIDCAVANGGCSDRCVNSPGFRCDCSDLYLHADGTGKATV-SCST 204

QY 288 -NDLCEHFVPPNPDPGYSYSCMCTGYRLADQHRCEVDVDCILEPSPCPQCVNTQGF 346

Db 205 DNGGCEHC-ENDSNGEYTRCGRVGFSLSEKSCQRPDPFDKGGCOHNTNNHRA 263

QY 347 ECHCYPNYDL-VDGCEVPEVPCFRAN-CEYQCPYLNQTSYLCVACGFPAPITHEPHRCQ 404

Db 264 QCCYCPFHLTYDRSCVDIDECANNGGCEHCENVKGT-YRCKREGV-QLGRDGRICE 321

QY 405 MF-----CNGTACPADC--DPTQASCCEPBGTYL----- 432

Db 322 EMLGGCQVNGGCGQHDYDQPDGHHVCKCRNGYILANDQKLCHDNISTVIHARAPRLMDS 381

QY 433 -----DDGF-----ICTDIDEC-ENGFCGVCVCH 455

Db 382 YETVTCVPTDITLTKLCHMLDLSGVQCFCDYGLYELIDSKFQDINECHENNGDSQICV 441

QY 456 NLPGTEFCICGPDLSAARHIGT-----DCDSKVDG-----DSGSGEPSPPTFGSTLY 505

Db 442 NLASGVCEQCKRGFLMKDRKTCEDISESSN--NGGCEQICSNQEGGVCSCERGFELS 499

QY 506 PPVAVG-----LVHSGLLIGTSLASLCLVALLALMLCHLRKKGAAAR-----AKM 549

Db 500 EDGHSCHDMNECLINNG-----GCAQLC-----KNRKSGRRCCQCFAGYILAMD 542

QY 550 EYKCAAPS 557

Db 543 EKSCVAAS 550

RESULT 6

A55567 fibrillin 1 - bovine

C/Species: *Bos primigenius taurus* (cattle)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: A55567

R/Title: D.U.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.

A/Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to

A/Reference number: A55567; MUID:95137597; PMID:7835900

A/Accession: A55567

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-2871 <F11>

A/Cross-references: UNIPROT:P98133; UNIPARC:UPI0000055AD2; GB:L28748; NID:9508427; PIDN:J

C/Superfamily: fibrillin; EGF homology

F.1201-1236/Domain: EGF homology <EGF>

Query Match 12.0%; Score 384; DB 2; Length 2871; Best Local Similarity 29.3%; Pred. No. 3e-15; Matches 129; Conservative 32; Mismatches 129; Indels 150; Gaps 25;

244 DCSYNGGCEHCNCAIIGARPCQCPAGALADGRSCTASTQSCNDLCEHFVNP----- 299

Db 1200 ECSIWNGGCEHFCNBSGYSYSCQCPGALMPDQSCST-----DIDE--CEDNPNICD 1250

QY 300 -----DQGSYSYSCMCTGYRLADQHRCEVDVDCILEBSPC-PQCVNTQGFEGHCYFN 353

Db 1251 GGQCTNIRGEYRCICVDGFMASEDMKTCVDVNECDLBNICLSGTCEHTKGSFICHDMG 1310

QY 354 YDLVDGE--CYEPVDP--FRANCEYQCPANQ--SYLCVABEFA-----PIPH 398

Db 1311 YSGKKGKGTCTD-INCECTIGANCDRAHACTNTAGSFKCSGSPWIGDGIKCTDLDECSN 1369

QY 399 EPHRCQMFQNTACPADCDPTQAS--CECEGYILDDGFICTDIDEC-EN----- 446

Db 1370 GTMCSQH-----ADC-KRTMGSYRLCLCEGY-TGGGFTCTDDESENLNCGNQC 1420

QY 447 ---GGF-----G--GVCHNLPGTECTCGPDSALAR 473

Db 1421 LNAPGYNRCEDMGFVPSADKACEDIDECSLPNICVGTGCHNLFGLRCEGCEIYEIDR 1480

QY 474 HIG-----TDCDSK-VDGDSGSEBPSPPTFGSTLYPPAVGLV--HSG----- 515

Db 1481 SGNCTDVNECLDPTTCTISGACVNTPGSYTDCDPPD---FELNTRGVCDVTRSGCYL 1536

QY 516 -----LHGISIASLCLVALLALMLCHLRKKGAAARA-----KMEYKC 553

Db 1537 DIRPAGNDGTRACSNIEIGVYSKASC-----GSLGAKMGPRCLCPVNTSEYKI 1587

QY 554 AAPSK-----VTLQHV 565

Db 1588 LCPGEGFRPNPITVYILEDI 1607

RESULT 7

A47221 fibrillin 1 precursor - human (fragment)

C/Species: *Homo sapiens* (man)
C/Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 31-Dec-2004

C/Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R/Accession: G.M.; Chabberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A/Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure

A/Reference number: A47221; MUID:94010947; PMID:7691719

A/Accession: A47221

A/Molecule type: mRNA

A/Residues: 1-337; T, 339-1029 <COR>

A/Cross-references: UNIPROT:P35555; UNIPROT:Q15972; UNIPROT:Q9NP01; UNIPARC:UPI000017651

A/Reference number: I54355; MUID:93372860; PMID:8364578

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 132-3002 <PBR>

A/Cross-references: UNIPARC:UPI0000055AD1; GB:J13923; NID:9306745; PIDN:AA02036.1; PID:

R.Maelen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
Nucleus 352, 334-337, 1991
A>Title: Partial sequence of a candidate gene for the Marfan syndrome.
A:Accession: S17064; MUID:91304568; PMID:1852207
A:Accession: S17064
A:Molecule type: mRNA
A:Residues: 1030-3002 <MAS>
A:Cross-references: UNIPARC:UPI0000176517; EMBL:X63556
R:Diez, H.C.; Valle, D.; Francemano, C.A.; Kendior, R.J.
Science 259, 680-683, 1993
A>Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A:Reference number: 159574; MUID:93157831; PMID:8430317
A:Accession: 159574
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 2217-2288, '1', 2290-2325 <RBS>
A:Cross-references: UNIPARC:UPI000006PFE6; GB:S54426; NID:9264860; PIDN:AA825244.1; PID:
R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfraz, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A>Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
A:Reference number: S17062; MUID:91304567; PMID:1852206
A:Accession: S17062
A:Molecule type: mRNA
A:Residues: 'VATVVFPLSYKML', 944-1444 <LEB1>
A:Cross-references: UNIPARC:UPI0000072A79; EMBL:X62008; NID:931398; PIDN:CA856534.1; PID:
A:Accession: S62111
A:Molecule type: Protein
A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEB2>
A:Cross-references: UNIPARC:UPI0000176518
R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A>Title: Connective tissue microfibrils. Isolation and characterization of three large F
A:Reference number: A34198; MUID:90078246; PMID:2512293
A:Accession: A34198
A:Molecule type: protein
A:Residues: 565-575, 1890-1892, 'T', 1894-1900 <MAD>
A:Cross-references: UNIPARC:UPI0000176519; UNIPARC:UPI000017651A
C:Comment: Fibrillin is a major component of elastin-associated microfibrils.
C:Genetics:
A:Gene: GDB:FBN1
A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700
A:Map position: 15q21.1-15q21.1
A:Insertions: 2236/1, 2258/1, 2297/1
C:Superfamily: EGF homology
C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted
F:132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MAD>
F:1332-1367/Domain: EGF homology <EGF2>
F:1457-1492/Domain: EGF homology <EGF2>
F:2262-2295/Domain: EGF homology <EGF1>

Query Match 12.0%; Score 384; DB 2; Length 3002;
Best Local Similarity 29.0%; Pred. No. 3.1e-15;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;

QY 244 DCSYENGGCEHAALPGARPCQCPAGALADGSCASTOSCNLDCEHFCVNP----- 299
DB 1331 ECSIINGGCEHFCVNPSESYSCSPGALMPDQSC-----DIE--CEDNPNICD 1381
QY 300 -----DQGSYSQMCETGYRLADQHRCEVDVDCILPSPC--PQCVNTQGFEGCHCYPN 353
DB 1382 GGQCTNIGEYRCLCYDFMASEBDMKTCVDVNECDLNPNICLSTGCENTKGSFICHDMG 1441
QY 354 YDVLVDE--CYEPVDP--FRANCEYQCPALNQT--SYLCVCAEGFA-----PIPH 398
DB 1442 YSGKKGKGTCTD--INECIGAHNGCKAVCTNTAGSFCSCSPGIGIGICTDLDECSN 1500
QY 399 EPHRCQMCNQACPADCDPTQAS--CECEGYLLDGFICTDIDEC--EN----- 446
DB 1501 GTNHCQH-----ADC-KITMGSYRCLCKEGY--TGSGFTCTDLDESENLNLCNGQC 1551
QY 447 ---GGF-----GS-----GVCNLPGTPECTCGPSALAR 473

DB 1552 LNAPGRCBCDMGFTVPSADKACEDIDECSLPNICVFETCNLPGLFRCECEIGYLD 1611
QY 474 HIG-----TDGSGKVDGDSGSGEPPEPTGS-----TLTPPAVGLV- 512
DB 1612 SGNCCTDVNECDLPTTCSGNV-----TGSYICDQCPPELNPTRVGCVD 1659
QY 513 -HSG-----LLIGISLCLVALLLCHLRKQGA-----A 545
DB 1660 TRSGNCYLDIRPGDNGDTACSNIEIGVYSKASC-----CSLGKAWGTPEMCPA 1710
QY 546 RAKMEYKCAAPSK-----VVLQHV 565
DB 1711 VNTSEYKILCPGEGFRPNPITVLEDT 1738

RESULT 8
A55624
fibrillin-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55624
R:Yin, W.; Smiley, E.; Garmiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez,
J. Biol. Chem. 270, 1798-1806, 1995
A>Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge
A:Reference number: A55624; MUID:95130561; PMID:7829516
A:Accession: A55624
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2871 <YIN>
A:Cross-references: UNIPROT:Q61554; UNIPARC:UPI00000289B6; GB:L29454; NID:9575509; PIDN:
C:Genetics:
A:Gene: Fbn-1
C:Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 11.9%; Score 382; DB 2; Length 2871;
Best Local Similarity 27.8%; Pred. No. 4e-15;
Matches 135; Conservative 31; Mismatches 148; Indels 172; Gaps 25;

QY 212 SAAVAIPGL-----QLMCTPRGAVGQHWARBARPGAMDGVENGGCEHAALPGARPC 265
DB 1162 SANLCPIHRCVNLIGKYQACANPGYHPTDRLFCVDIDECISIMNGGCEFTTNSDSEYC 1221
QY 266 QCPAGALADGSCASTOSCNLDCEHFCVNP-----DQGSYSQMCETGYRLA 316
DB 1222 SCQGFALMPDQSC-----CEDNPNICDGGCTNIPESYRCLCYDFMAS 1272
QY 317 ADQHRCEVDVDCILPSPC--PQCVNTQGFEGCHCYPNYDLVDE--CYEPVDP--FRA 371
DB 1273 EDMKTCVDVNECDLNPNICLSTGCENTKGSFICHDMGYSKKKGTGCTD--INCEIGAH 1331
QY 372 NCEYQCPALNQT--SYLCVCAEGFA-----PIHBRQCFNQTACPADCDPNT 420
DB 1332 NCGHNAVCTNTAGSFCSCSPGWIIGDICTDLDECSNHTMCSQH-----ADC--KNT 1383
QY 421 QAS--CECEGYLLDGFICTDIDEC--EN-----GGF----- 449
DB 1384 MGSYRCLCKQGY--TGSGFTCTDLDESENLNLCNGQCLNAPGYSRCBCEMDGFTVPSADG 1442
QY 450 -----CS-----GVCNLPGTPECTCGPSALARHIG-----TDGSGKV 484
DB 1443 ACEDIDECSLPNICVFETCNLPGLFRCECEIGYELDRSGNCTDVNECDLPTTCSGNC 1502
QY 485 DGDGSGGEPPEPTGS-----TLTPPAVGLV--HSG----- 515
DB 1503 VN-----TPGSYICDQCPPELNPTRVGCVDTSNGCYLNIRPGDNGDTACS 1550
QY 516 -LLIGISLCLVALLLCHLRKQGA-----ARAMEYKCAAPSK----- 559
DB 1551 NEIGVYSKASC-----CSLGKAWGTPELCPSTVNTSEYKILCPGEGFRPNPIT 1601
QY 560 VVLQHV 565

Db 1602 VILEDI 1607

RESULT 9

A57278
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: A57278
R:Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A:Title: Developmental expression of fibrillin gene suggests heterogeneity of extracellular matrix
A:Reference number: A57278; MUID:95263670; PMID:7744963

A:Accession: A57278
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2907 <ZNA>

A:Cross-references: UNIPROT:O61555; UNIPARC:UPI0000028989; GB:L39790; NID:G762830; PIDN: F1239-1274/Domain: EGF homology <EGF1>
F12488-2523/Domain: EGF homology <EGF>

Query Match 11.7%; Score 374.5; DB 2; Length 2907;
Best Local Similarity 33.0%; Pred. No. 1,1e-14;
Matches 102; Conservative 24; Mismatches 92; Indels 91; Gaps 18;

Qy 244 DCSYENGSCHEACNAIPGAPQCAGALQADGSCSTASTQSCNDLCEHFCVNPDP--- 300
Db 1238 EGMINGGCDPQCTNSBGSYSCSSEGYALMPDRSCA-----DIDE--CENNPDI CD 1288
Qy 301 -----QGSYSYSCETGYRLADQHRCEVDVDCILESPCP-ORCVNTQGGFCHCYPN 353
Db 1289 GGQCTNIGEYRCICLYGDFPMASMDKTCIDVNECDLNSNLCMFGECEWTKGSFICHQQLG 1348
Qy 354 YDLVDGE--CYEPVDP--FRANCEYOCQPLN-QTSYLCVCAEGFA-----PIPH 398
Db 1349 YSVKGGTGTCTD-VDECEIGAHNCMDHASCINPVSFPCSCREGVNGIKICIDDECAN 1407
Qy 399 BPHRCQMCNCPADCDPNTQAS--CECPGTYLDDGFICTDIDE-----CENG-- 447
Db 1408 GTHQCSI-----NAQC-VNTPGSRACSEGF-TGQGFCTSDVDECAENINLCENGC 1458
Qy 448 -----GF-----CS-----GVCNLPETFEICGPPSALAR 473
Db 1459 LNVPGAYRCECEMGFTPADSRSCODIDCSFQNICVPTCNMLGMPHCICIDDEYELDR 1518
Qy 474 HIG--TDGD 480
Db 1519 TGGNCTDID 1527

RESULT 10

A54105
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A54105; S17063; S31101
R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanginetti, C.; Bonadio, J.; Mecham, J. Cell Biol. 124, 855-863, 1994
A:Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefe
A:Reference number: A54105; MUID:94165150; PMID:8120105

A:Accession: A54105
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2918 <ZNA>

A:Cross-references: UNIPROT:P35556; UNIPARC:UPI000017651B; GB:U03772
R:Lee, B.; Godfrey, W.; Vitale, E.; Hori, H.; Mattei, M.G.; Safarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe
A:Reference number: S17063; MUID:91304567; PMID:1852206

A:Accession: S17063
A:Molecule type: mRNA
A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLT', 1922-1923, 'LD', 1926, 'P', 1928 <LEB>

A:Cross-references: UNIPARC:UPI000017651C; EMBL:X62009
R:Milwicz, D.M. EMBL Data Library, December 1992
A:Reference number: S31101
A:Accession: S31101
A:Molecule type: mRNA
A:Residues: 752-1407, 'R', 1409-1489, 1791, 'GS', 1794-1796, 'QLT', 1922-1923, 'LD', 1926, 'P', 1928
A:Cross-references: UNIPARC:UPI000000069B; EMBL:X62009

A:Gene: GDB:FBN2
A:Cross-references: GDB:128122; OMIM:121050
A:Map position: 5q23-5q31
C:Superfamily: fibrillin; EGF homology
C:Keywords: extracellular protein
F1-29/Domain: signal sequence #status predicted <SIG>
F130-2918/Product: fibrillin-2 #status predicted <MNT>
F1245-1280/Domain: EGF homology <EGF1>
F1970-2013/Domain: EGF homology <EGF>

Query Match 11.7%; Score 373.5; DB 2; Length 2918;
Best Local Similarity 29.9%; Pred. No. 1.3e-14;
Matches 118; Conservative 34; Mismatches 124; Indels 119; Gaps 21;

Qy 244 DCSYENGSCHEACNAIPGAPQCAGALQADGSCSTASTQSCNDLCEHFCVNPDP--- 300
Db 1244 EGMINGGCDPQCTNSBGSYSCSSEGYALMPDRSCA-----DIDE--CENNPDI CD 1294
Qy 301 -----QGSYSYSCETGYRLADQHRCEVDVDCILESPCP-ORCVNTQGGFCHCYPN 353
Db 1295 GGQCTNIGEYRCICLYGDFPMASMDKTCIDVNECDLNSNLCMFGECEWTKGSFICHQQLG 1354
Qy 354 YDLVDGE--CYEPVDP--FRANCEYOCQPLN-QTSYLCVCAEGFAPIPH-----EPHRC 403
Db 1355 YSVKGGTGTCTD-VDECEIGAHNCMDHASCINPVSFPCSCREBGM--IGNIKICIDDECE 1411
Qy 404 QMPCNCPADCDPNTQAS--CECPGTYLDDGFICTDIDE-----CENG----- 447
Db 1412 SNGHQCISNAQC-VNTPGSRACSEGF-TGQGFCTSDVDECAENINLCENGCCLAVPG 1469
Qy 448 -----GF-----CSGVCNLPETFEICGPPSALARHIG-- 476
Db 1470 AYRCCEBGFPTPADSRSCODIDCSFQNICVSGTCNNLPMPHFICIDDEYELDRGTGNC 1529
Qy 477 TDCSGKATDGDSSGGEPPSP-----TGSTLTTPAVLV----- 512
Db 1530 TDIDE-CADPINCYNGLCVNTPGRYECNCPDPFQINPVGVCVNRVNCYLKFGPRGDG 1588
Qy 513 -----HSGLLIGISTASLCLVALALCHLRKXG 543
Db 1589 SLSCNTEIGVGSRSRSC-----CSLGRKMG 1614

RESULT 11

A55184
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: A55184; T08744
R:Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.
Genomics 22, 445-430, 1994
A:Title: Fibrillin-2 (FBN2): human cDNA sequence, mRNA expression, and mapping of the gen
A:Reference number: A55184; MUID:95104855; PMID:7806230

A:Accession: A55184
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1184 <ZNA>

A:Cross-references: UNIPROT:P98095; UNIPARC:UPI000012A567; GB:X82494; NID:9575232; PIDN: R:Wambut, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999

A:Reference number: Z16471
A:Accession: T08744
A:Molecule type: mRNA

A:Residues: 656-719, 'QDECLMGHSDSRQPCVNTGSPFCVNHVTLACADGYTLNHRKCV', 720-853, 'T', 855-11
A:Crosss-references: UNIPARC:UPI00000673AD; EMBL:AL050095
A:Experimental source: adult uterus; clone DKFZp586a1519
C:Genetics:
A:Gene: GDB:FBLN2
A:Crosss-references: GDB:293037; OMIM:135821
A:Map position: 3p25-3p24
A:Note: DKFZp586a1519.1
C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology
C:Keywords: alternative splicing; extracellular matrix
F:1-37/Domain: signal sequence #status predicted <SIG>
F:128-1184/Product: fibulin-2 protein #status predicted <MAT>
F:905-941/Domain: EGF homology <EGF>

Query Match 11.3%; Score 363; DB 2; Length 1184;
Best Local Similarity 29.7%; Pred. No. 2, 6e-14;
Matches 118; Conservative 29; Mismatches 124; Indels 126; Gaps 21;

QY 154 EEOQCEVAD-GFLCEHFPATC-----RPLAV-----EPGAAAAYSITVGPFAARG 201
DB 531 EGQSCSNPNLGYPCN-HVMTSCGGEPLIVPEVRRPPEAARVVS-----EAMM 582
QY 202 ADFQALPVGSSAAV---APLGLQMLCTAPRGAVQGHMARBARAGANDCSVENGCSEHACNA 258
DB 583 AGREALSTGEHELPNLSLPGDDQDECLLPGL-----COHLCTIN 622
QY 259 IFGARPCCPAGALQADGRSC-----TAST-----QS 286
DB 623 TVGSHYACFPQFSIQDDGRTKRPGRHPQRPAPBPALPKSRQVASTNTPPLPQRYNT 682
QY 287 CND--LCEHFCVNPDPQSGYSCMCETGYRLAADGRCEVDVDCILESPCP--QRVNT 342
DB 683 CKDNQPCQKVC---STVGSAISCFCPGYAIWADVSCEDINECVTDLHTCSRGSHCVNT 739
QY 343 QCGFECH---CYRNYDIVGECVPEVPDPCFRANECYOCPLANQSYLCV----- 388
DB 740 LGSFPCYALATCEPGYALKDEGC-BDVDEC--AMGTHTCQ---GFLCQNTKSGPYCOA 792
QY 389 ---CAEGFAPIPH-----BPHRCQMFNQTACPADCDPNTQASCEPBGY-I 431
DB 793 RQRCMDGLDPBEGKNCVINECTSLSECRPEFSCTINTVGSYTCORNPULI---CARGYHA 849
QY 432 LDDGFTCTDIDECENGFCSCG---VCHNLPGETFECIC 465
DB 850 SDDGAKCVDVNECETGVHRCGEGYCHNLPGSYRDC 886

RESULT 12
T46488
hypochemical protein DKFZp434J065.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46488
R:Diesterheft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223035
A:Accession: T46488
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-741 <AAA>
A:Crosss-references: UNIPROT:O8NDE6; UNIPARC:UPI000016ACGB; EMBL:AL137638
A:Experimental source: adult testis; clone DKFZp434J065
C:Genetics:
A:Note: DKFZp434J065.1

Query Match 11.2%; Score 358.5; DB 2; Length 741;
Best Local Similarity 31.6%; Pred. No. 3, 2e-14;
Matches 86; Conservative 40; Mismatches 101; Indels 45; Gaps 15;

QY 245 CSVENGCSEHACNAIPGARPCCPAGALQADGRCTA--STQSCNDLCEHFCVNPDP 302
DB 68 CAMEDHNCBQLCVNPGSFVQCYSYGVALAEDGKRCVAVDYCASBNHCSEHCV-NAD-- 124

QY 303 GSYSCMCETGYRLAADGRCEVDVDCILESPBPQRCVNTQGGFECHCYPNVDL-VDGEC 361
DB 125 GSYLCQCHGEPALNDEKTCIKYIDYCASBNHCQCHCVNTDYSCHCLKGFTLNPDKT 184
QY 362 VEPDPCF--RANCYQOQPLANQSYLCVCAEGFAPIPH-----EPHCCQFC 407
DB 185 CRRIYCALNPGGCHECVNMNEB-SYRCRHRGYLTDNGKTCRSRDHCAQODHCEQLC 243
QY 408 NOTACPADCDPNTQAS--CECPGTYLDDGF-ICTDIDEC---ENGFCSGVCHNLPGETF 461
DB 244 -----LNTBSPFCQCSBGFILNEDLKTGRVDYCLSDHG--CEYSCVMNDSF 291
QY 462 ECTCGPDSALARIHITGDCDSGRVDG---GDGSG 490
DB 292 ACQC-PBGHVLRSQDKTC--AKLDSCALGDHG 320

RESULT 13
A49457
fibulin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A49457; S74095
R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Paessler, R.; Timpl, R.; Chu, M.L.
J. Cell Biol. 123, 1269-1277, 1993
A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein wit
A:Reference number: A49457; MUID:94064787; PMID:8245130
A:Accession: A49457
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1221 <PAN>
A:Crosss-references: UNIPROT:P37889; UNIPARC:UPI000029929; GB:X75285; NID:9437046; PIDN:
R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
Eur. J. Biochem. 240, 427-434, 1996
A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix met
A:Reference number: S74094; MUID:96439073; PMID:8841408
A:Accession: S74095
A:Molecule type: protein
A:Residues: 236-238 'X', 240-247, 260-275, 336-344, 'L', 346-361, 405-426, 566-568, 'EW', 569-589
A:Crosss-references: UNIPARC:UPI0000176509; UNIPARC:UPI000017650A; UNIPARC:UPI000017650B;
510; UNIPARC:UPI0000176511; UNIPARC:UPI0000176512
C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology
C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
F:942-978/Domain: EGF homology <EGF>

Query Match 11.1%; Score 356.5; DB 2; Length 1221;
Best Local Similarity 29.5%; Pred. No. 6, 4e-14;
Matches 123; Conservative 39; Mismatches 140; Indels 115; Gaps 27;

QY 154 EEOQCEVAD-GFLCEHFPATC-----RPLAV-----EPGAAAAYSITVGPFAARG 192
DB 521 EGQSCSNPNLGYPCN-HVMTSCGGEPLIVPEVRRPPEAARVVS-----EAMM 579
QY 193 YGT---PFAARGADPQ---ALP-----VGSAAVAAPLGLQML---CTAPPG 229
DB 580 LGTEBELPNLSLPGDDQDECLLPGLCQHLCTINTVGSYRACFPGBFLQGDGRTCRPDG 639
QY 230 AVQGHMARE-APGAMDCSY-----ENGGECHACNAIPGARPCCPAGAA 272
DB 640 APQDITAEAPRBSAQSVPNTIPLPVDPNTCKDNGPCQGVCRVAGDITAMCSGFPGYA 699
QY 273 LQADGRS-----CTASTOSGNDLCEHFCVNPDPQSGYSC-----MCETGYRLAADGR 321
DB 700 IMADGVSCEDDDECLMGTHDS--WKQPCV---NTLGSFYCVNHTVLCABEYIILNA-HRK 753
QY 322 CEDVDCLLESPC--PQRCVNTQGGFECH---CYRNYDIVGECVPEVPDPCFRA--NC 373
DB 754 CVDINECVTDLHTCTRAHNCVNTPGSFQCYALATCEPGYVLTDECTD-VDECVGTATNC 812
QY 374 E--YQOQPLNQTSTLCV---CAGGFAPIPH-----BPHRCQMFNQTACPA 414
DB 813 QAGSGCN-TKSGPYCOARQRCMDGFLQDPBEGKNCVINECTSLLEPGRSGFSCTINTVGSY 871

QY 415 DCDPNTQASCEBPGY-ILDDGFICTDIDECENGFCGSG---VCHNLPGTECTIGP 467
Db 872 TCQGNPLV---CGGHYANNEGSCVDVNECECTGHRGEGQLCYNLPGSYRCDCKP 925

RESULT 14

A38261
masking protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C:Accession: A38261
R:Thuji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990
A:Title: Molecular cloning of the large subunit of transforming growth factor type beta
A:Reference number: A38261; MUID:91062373; PMID:2247454
A:Accession: A38261
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1712 <TSU>
A:Cross-references: UNIPROT:Q00918; UNIPARC:UPI000012B99B; GB:M55431; NID:9207285; PIDN:
F:911-947/Domain: EGF homology <EGF>

Query Match 10.4%; Score 333; DB 2; Length 1712;

Best Local Similarity 29.0%; Pred. No. 2,1e-12;

Matches 107; Conservative 44; Mismatches 130; Indels 88; Gaps 27;

QY 177 PLAVEPGAAAVSTYGTFFAAGADFOALPVGS---SAAVAPLGLQLM--CTAPPGA 230
Db 831 PVVEKTSPPVPEVA-----PEGSTSASQVIAPVTEINECTVNDI 875
QY 231 VQGHMAREAPGAMDCSVENG-----GCEHA-----CNAIPGARPCQCP 268
Db 876 CGAGHCILPVRVYCTICEGVKFSQKRCIDIDECQAQOHLCSQRCENTEGSFLCICP 935
QY 269 AGAALQADGRCTASTGSC--NDLC-EHFCVNPNPQPSYSC-METGYRLAADHRCED 324
Db 936 AGFLASEGSSNC-IDVDCLRPDYCRDRCI--NTAARFCEYDCSGRMSRRGH-CED 990
QY 325 VDDCLLESPCP-ORCVNTQSGFEC-HCYPNYDLVDSGVBPVDPCCFAN--CEYQCP 380
Db 991 IDECLTPTSTCEBECVNSPGSYQCVPTCEGFRGNQCLD-VDDECLQPKVCTNSCTNL 1048
QY 381 NOTSYLCVAGAFAPRPH-----RCQM--FCNQTACPADCDPNTQAS--CECPGYI 431
Db 1049 -EGSYMGSCHKYSPTPRHRHCQDIDECQGNLCNNGQC-----KNTDGSFRCTCGQGYQ 1102
QY 432 L---DGFICTDIDECENGFCG--GVCHNLPGTECTIGPD---SALARHIG--TDC-- 479
Db 1103 LSAADQ---CEDIDECERHLCSHGQCRNTEGSPCLCNQGYRASVLGDHCEDINECLE 1159
QY 480 DSGKVDGD 488
Db 1160 DSSVCGGD 1168

RESULT 15

T43210
fibulin-1D precursor - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Apr-2004

C:Accession: T43210

R:Barth, J.L.; Argaves, K.M.; Roark, E.F.; Little, C.D.; Argaves, W.S.
submitted to the EMBL Data Library, June 1998

A:Description: Identification of chicken and C. elegans fibulin-1 homologs and character

A:Reference number: Z22337

A:Accession: T43210

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-589 <BAB>

A:Cross-references: UNIPARC:UPI000016B67E; EMBL:AF070477; PIDN:AAC24035.1

C:Genetics:
A>Note: intron positions not resolved (incomplete sequence)

Query Match 10.3%; Score 330.5; DB 2; Length 589;
Best Local Similarity 28.2%; Pred. No. 1.2e-12;
Matches 125; Conservative 49; Mismatches 172; Indels 97; Gaps 27;

QY 103 GPLRGF-QWLTGDNNTSRRARLDLNGAPLCPGLCAVSAABEATVSEPT-----WEEQ 156
Db 19 GCLRSFNKCCNGDLEITH---ASEITGRPLNDPHVHLHGRCSHCHCHGRGKXV 75
QY 157 QCEVKA-----DGLCEFHFP--ATCRPLAVE-----PGAAAAVSTYGTFFA--- 198
Db 76 ECSCRSGFDLAPDGMACVDHIDECATLMDCLIESQRCINTPGSFCTIRTLSCGYANDS 135
QY 199 --AGADPQALPVSSAAVAPLGLQMLCTAPGAVQ-----GHMAREAPGAMDCS--- 246
Db 136 ETERCRVDCECNLSH---DCGPLYOCRTQSSRYCDACKKGSGELQNPMTGECTISITC 191
QY 247 -----VENGCE-----HACNA-----IPGARPCQCPAGAAALQADGRCTASTQSC 287
Db 192 PNGYPRKMGNDIDECVTGHNCGAGBECVNTPESPFCQKGN--LCAHYEVNAGATGFC 249
QY 288 NDL--CEH-----FCVNPDPQPSYSCMETGYRLAADHRCEDVDDCLV---EPSEFCP 336
Db 250 EDVNECOQVCGSMECI--NLPGTYKCKCGPYEFNDAKKRCBVDDECIFAGHVCDSL 306
QY 337 ORCVNTQSGFECCHCPNVDLV-DGCVBPVDPCCR--ANCEYQCPPLNQTSYLCVCAEGF 393
Db 307 AECINTIGSFPECKKPFQALSDGRCEVDNECTTGIAACQKCVNI--PGSYQCTCDRGF 365
QY 394 APIP-----HEPRHCOMFC--NOTACPADCDPNTQAS--CECPGY-ILDDGFICTDIDE 443
Db 366 ALGPDGTCEIDIDECSTIAGSGNDLCMGCC--INTKGYLCCGCPGYKIQPGGRICVDVDE 424
QY 444 CENGFGCGS---VCHNLPGTEFC 463
Db 425 CAMGE-CAGSDKVCNTLGSFKC 446

Search completed: February 4, 2006, 04:32:59
Job time : 47 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using SW model

Run on: February 4, 2006, 04:32:27 ; Search time 51 Seconds

(without alignments)
930.507 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MGVLTGALALAGLGPAP.....APSKVVIQHVTRTPQRL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/BCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	3176.5	99.2	575	1 US-08-312-870-1	Sequence 1, Appli
2	3176.5	99.2	575	2 US-09-949-002-296	Sequence 296, App
3	3176.5	99.2	575	6 5466668-6	Patent No. 5466668
4	3176.5	99.2	682	2 US-09-949-002-436	Sequence 436, App
5	3172.5	99.0	575	1 US-08-261-206A-59	Sequence 59, Appl
6	3172.5	99.0	575	2 US-09-880-484D-2	Sequence 2, Appli
7	3172.5	99.0	575	2 US-10-438-648-2	Sequence 2, Appli
8	3168.5	98.9	575	1 US-08-170-290A-54	Sequence 54, Appl
9	3107	97.0	572	6 5256770-7	Patent No. 5256770
10	2885.5	90.1	516	2 US-09-509-994-2	Sequence 2, Appli
11	2881.5	90.0	516	2 US-09-509-994-1	Sequence 1, Appli
12	2795.5	87.3	498	1 US-08-733-564-2	Sequence 2, Appli
13	2793.5	87.2	497	1 US-08-312-870-3	Sequence 3, Appli
14	2789.5	87.1	497	2 US-09-331-793-4	Sequence 4, Appli
15	2735.5	85.4	494	1 US-08-014-723-14	Sequence 14, Appl
16	2735.5	85.4	494	1 US-08-110-011A-14	Sequence 14, Appl
17	2733.5	85.3	494	1 US-08-014-723-16	Sequence 16, Appl
18	2733.5	85.3	494	1 US-08-110-011A-16	Sequence 16, Appl
19	2659.5	83.0	475	1 US-08-307-444A-2	Sequence 2, Appli
20	2659.5	83.0	475	1 US-08-587-389-2	Sequence 2, Appli
21	2655.5	82.9	475	1 US-08-307-444A-1	Sequence 1, Appli
22	2655.5	82.9	475	1 US-08-587-389-1	Sequence 1, Appli
23	2649.5	82.7	476	1 US-08-014-723-1	Sequence 1, Appli
24	2649.5	82.7	476	1 US-08-110-011A-1	Sequence 1, Appli
25	2647.5	82.7	476	1 US-08-014-723-2	Sequence 2, Appli
26	2647.5	82.7	476	1 US-08-014-723-18	Sequence 18, Appl
27	2647.5	82.7	476	1 US-08-110-011A-2	Sequence 2, Appli

28	2647.5	82.7	476	1 US-08-110-011A-18	Sequence 18, Appl
29	2565.5	80.1	456	1 US-08-307-444A-4	Sequence 4, Appli
30	2565.5	80.1	456	1 US-08-587-389-4	Sequence 4, Appli
31	2561.5	80.0	456	1 US-08-307-444A-3	Sequence 3, Appli
32	2561.5	80.0	456	1 US-08-587-389-3	Sequence 3, Appli
33	2512.5	78.4	446	1 US-08-307-444A-5	Sequence 5, Appli
34	2512.5	78.4	446	1 US-08-587-389-5	Sequence 5, Appli
35	1590.5	49.7	245	1 US-08-312-870-7	Sequence 7, Appli
36	1323	41.3	239	2 US-10-104-047-2759	Sequence 2759, Ap
37	1159	36.2	215	1 US-08-312-870-5	Sequence 5, Appli
38	689	21.5	115	1 US-08-312-870-9	Sequence 9, Appli
39	681	21.3	114	1 US-08-733-564-1	Sequence 1, Appli
40	587.5	18.3	652	1 US-08-751-305-2	Sequence 2, Appli
41	578	18.0	757	2 US-09-949-016-6963	Sequence 6963, Ap
42	578	18.0	758	2 US-09-949-016-8087	Sequence 8087, Ap
43	573	17.9	492	2 US-09-724-864-39	Sequence 39, Appl
44	384	12.0	1935	2 US-09-949-092-10403	Sequence 10403, A
45	384	12.0	2871	2 US-09-538-092-1076	Sequence 1076, Ap

ALIGNMENTS

RESULT 1
US-08-312-870-1
; Sequence 1, Application US/08312870
; Patent No. 5639625
; GENERAL INFORMATION:
; APPLICANT: Carson, Craig W.
; TITLE OF INVENTION: Method for Detecting Antibodies to
; TITLE OF INVENTION: Thrombomodulin in Patients
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richards, Medlock & Andrews
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: Texas
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/312,870
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hansen, Eugenia S.
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: OMRF B35150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: Protein
; LOCATION: 19..575
; US-08-312-870-1
Query Match 99.2%; Score 3176.5; DB 1; Length 575;
Best Local Similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
DB 1 MLGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
QY 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120
DB 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120
QY 121 RWARLDINGAPLCGFLCVAVSAEAATVSEPIWEBOQCEVKADGFLCEHFHPTATCRPLAV 180
DB 121 RWARLDINGAPLCGFLCVAVSAEAATVSEPIWEBOQCEVKADGFLCEHFHPTATCRPLAV 180
QY 181 EPGAAAIAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHAREAP 240
DB 181 EPGAAAIAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHAREAP 240
QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
QY 300 DQPGSYSCMCEGYRLADQHRCEVDVDCILBSPCPCRCVNTQGGFCHCYPNYDLVDG 359
DB 301 DQPGSYSCMCEGYRLADQHRCEVDVDCILBSPCPCRCVNTQGGFCHCYPNYDLVDG 359
QY 360 ECVEPVDCFPANACEYQCPINQTSYLCVABGFAPIPHEPHRCMFCNQACPADCDPN 419
DB 361 ECVEPVDCFPANACEYQCPINQTSYLCVABGFAPIPHEPHRCMFCNQACPADCDPN 419
QY 420 TQASCECEGYLLDDGFLCTDIDECENGFCGVCCHNLPGTPECICGPDALARIHIGTDC 479
DB 421 TQASCECEGYLLDDGFLCTDIDECENGFCGVCCHNLPGTPECICGPDALARIHIGTDC 479
QY 480 DSGKVDGDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCVALLALCHLR 539
DB 481 DSGKVDGDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCVALLALCHLR 539
QY 540 KKGGAARAMEYKCAAPSKVVLQHVTRTERTPORL 574
DB 541 KKGGAARAMEYKCAAPSKVVLQHVTRTERTPORL 574

RESULT 2
US-09-949-002-296
Sequence 296, Application US/09949002
Patent No. 5900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: C1000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 296
LENGTH: 575
TYPE: PRT
ORGANISM: Human
US-09-949-002-296

Query Match 99.2%; Score 3176.5; DB 2; Length 575;
Best Local Similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
DB 1 MLGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
QY 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120

DB 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120
QY 121 RWARLDINGAPLCGFLCVAVSAEAATVSEPIWEBOQCEVKADGFLCEHFHPTATCRPLAV 180
DB 121 RWARLDINGAPLCGFLCVAVSAEAATVSEPIWEBOQCEVKADGFLCEHFHPTATCRPLAV 180
QY 181 EPGAAAIAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHAREAP 240
DB 181 EPGAAAIAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHAREAP 240
QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
QY 300 DQPGSYSCMCEGYRLADQHRCEVDVDCILBSPCPCRCVNTQGGFCHCYPNYDLVDG 359
DB 301 DQPGSYSCMCEGYRLADQHRCEVDVDCILBSPCPCRCVNTQGGFCHCYPNYDLVDG 359
QY 360 ECVEPVDCFPANACEYQCPINQTSYLCVABGFAPIPHEPHRCMFCNQACPADCDPN 419
DB 361 ECVEPVDCFPANACEYQCPINQTSYLCVABGFAPIPHEPHRCMFCNQACPADCDPN 419
QY 420 TQASCECEGYLLDDGFLCTDIDECENGFCGVCCHNLPGTPECICGPDALARIHIGTDC 479
DB 421 TQASCECEGYLLDDGFLCTDIDECENGFCGVCCHNLPGTPECICGPDALARIHIGTDC 479
QY 480 DSGKVDGDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCVALLALCHLR 539
DB 481 DSGKVDGDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCVALLALCHLR 539
QY 540 KKGGAARAMEYKCAAPSKVVLQHVTRTERTPORL 574
DB 541 KKGGAARAMEYKCAAPSKVVLQHVTRTERTPORL 574

RESULT 3
546668-6
Patent No. 546668
APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
DAVID R.
TITLE OF INVENTION: SUPERIOR THROWMODULIN ANALOGS FOR
PHARMACEUTICAL USE
NUMBER OF SEQUENCES: 57
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,346
FILING DATE: 22-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 568,456
FILING DATE: 15-AUG-1990
APPLICATION NUMBER: 506,325
FILING DATE: 09-APR-1990
APPLICATION NUMBER: 406,941
FILING DATE: 13-SEP-1989
APPLICATION NUMBER: 345,374
FILING DATE: 28-APR-1989
SEQ ID NO: 6
LENGTH: 575
546668-6

Query Match 99.2%; Score 3176.5; DB 6; Length 575;
Best Local Similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
DB 1 MLGVLVITGALALAGIFPAPAPBPQGSQCVBHDCEALYPGPATPLNASQICDGLRGHLM 60
QY 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120
DB 61 TVRSSVAADVISLLINGDGVGRRRLMTGLQLPFCGCBPKRLGPIRGFQWVTGDNNTSYS 120
QY 121 RWARLDINGAPLCGFLCVAVSAEAATVSEPIWEBOQCEVKADGFLCEHFHPTATCRPLAV 180

Db 121 RMARLDLNGAPLCPGLCAVSAAEATVSEPIWEEQCEVKADGFLCEHFPAICRPLAV 180
Qy 181 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
Db 181 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
Qy 241 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
Db 241 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITASATQSCNDLCEHFCVNP 300
Qy 300 DPGSYSCMCEGTGYLAADQHRCEVDCCILBSPQRCVNTQGFECHECPNPDVNG 359
Db 301 DPGSYSCMCEGTGYLAADQHRCEVDCCILBSPQRCVNTQGFECHECPNPDVNG 360
Qy 360 ECEVVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDN 419
Db 361 ECEVVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDN 420
Qy 420 TQASCECEGYLLDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCECEGYLLDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 480
Qy 480 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 481 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
Qy 540 KKGGAARAMEYKCAAPSKVVLQHVTRTERPQRL 574
Db 541 KKGGAARAMEYKCAAPSKVVLQHVTRTERPQRL 575

RESULT 4

US-09-949-002-436
; Sequence 436, Application US/09949002
; Patent No. 6300016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-436

Query Match 99.2%; Score 3176.5; DB 2; Length 682;
Best Local Similarity 99.5%; Pred. No. 5-5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MLGVIVLICALALAGIAPAPAPAPGSGQCVENHDFALYPGATTLNLSQICDGLRGHLM 60
Db 108 MLGVIVLICALALAGIAPAPAPAPGSGQCVENHDFALYPGATTLNLSQICDGLRGHLM 167
Qy 61 TVRSSVADVITSLINGGVGRRLMTGLQIPPCGDPKRLGRLRGQWVTGDNNTSYS 120
Db 168 TVRSSVADVITSLINGGVGRRLMTGLQIPPCGDPKRLGRLRGQWVTGDNNTSYS 227
Qy 121 RMARLDLNGAPLCPGLCAVSAAEATVSEPIWEEQCEVKADGFLCEHFPAICRPLAV 180
Db 228 RMARLDLNGAPLCPGLCAVSAAEATVSEPIWEEQCEVKADGFLCEHFPAICRPLAV 287
Qy 181 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
Db 288 EPGAAAAAASITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 347

Qy 241 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
Db 348 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITASATQSCNDLCEHFCVNP 407
Qy 300 DPGSYSCMCEGTGYLAADQHRCEVDCCILBSPQRCVNTQGFECHECPNPDVNG 359
Db 408 DPGSYSCMCEGTGYLAADQHRCEVDCCILBSPQRCVNTQGFECHECPNPDVNG 467
Qy 360 ECEVVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDN 419
Db 468 ECEVVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDN 527
Qy 420 TQASCECEGYLLDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 479
Db 528 TQASCECEGYLLDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 587
Qy 480 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 588 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 647
Qy 540 KKGGAARAMEYKCAAPSKVVLQHVTRTERPQRL 574
Db 648 KKGGAARAMEYKCAAPSKVVLQHVTRTERPQRL 682

RESULT 5

US-08-261-206A-59
; Sequence 59, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Birch, Stewart, Kolaesch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELE: 248345
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..575
OTHER INFORMATION: /label= protein
OTHER INFORMATION: /note= "human thrombomodulin"
US-08-261-206A-59
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Query Match          99.0%; Score 3172.5; DB 1; Length 575;
Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 1 MLGVLVIGALALAGLGGPPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLGGPPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVADVISLLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGQWVTGDNNTSYS 120
DB 61 TVRSSVADVISLLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGQWVTGDNNTSYS 120
QY 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
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DB 181 EPGAALAAVSTTGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
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DB 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
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DB 300 DQPGSYCMCTGYRLADQHRCEVDVDCILEPSPQRCVNTQGFECCHCPNYDLVDG 359
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DB 360 ECVEVPDPCFRANCEYQCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQACPADCPN 419
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DB 480 DSGKVDGSDSGSGRPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
QY 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPQRL 574
DB 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPQRL 574
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RESULT 6
US-09-880-484D-2
Sequence 2, Application US/09880484D
Patent No. 6632791
GENERAL INFORMATION:
APPLICANT: Light, David
APPLICANT: Nagashima, Mariko
APPLICANT: Morser, Michael J
TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
FILE REFERENCE: 51863AUSM1
CURRENT APPLICATION NUMBER: US/09/880,484D
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/213,678
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 575
TYPE: PRT
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ORGANISM: Homo sapiens
US-09-880-484D-2
Query Match          99.0%; Score 3172.5; DB 2; Length 575;
Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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DB 1 MLGVLVIGALALAGLGGPPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVADVISLLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGQWVTGDNNTSYS 120
DB 61 TVRSSVADVISLLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGQWVTGDNNTSYS 120
QY 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
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DB 181 EPGAALAAVSTTGTTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
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DB 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
QY 300 DQPGSYCMCTGYRLADQHRCEVDVDCILEPSPQRCVNTQGFECCHCPNYDLVDG 359
DB 300 DQPGSYCMCTGYRLADQHRCEVDVDCILEPSPQRCVNTQGFECCHCPNYDLVDG 359
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DB 360 ECVEVPDPCFRANCEYQCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQACPADCPN 419
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DB 420 TQASCECEGYILDDGFLCTDIDECENGFGSGVCHNLPGTRECICGPDLSALVRIHIGDC 479
QY 480 DSGKVDGSDSGSGRPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
DB 480 DSGKVDGSDSGSGRPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
QY 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPQRL 574
DB 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPQRL 574
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RESULT 7
US-10-438-648-2
Sequence 2, Application US/10438648
Patent No. 6790828
GENERAL INFORMATION:
APPLICANT: Light, David
APPLICANT: Nagashima, Mariko
APPLICANT: Morser, Michael J
TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
FILE REFERENCE: 51863AUSD1
CURRENT APPLICATION NUMBER: US/10/438,648
PRIOR FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US 60/213,678
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 09/880,484
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 575
TYPE: PRT
ORGANISM: Homo sapiens
US-10-438-648-2
Query Match          99.0%; Score 3172.5; DB 2; Length 575;
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Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 1 MLGVVLGALALAGLPAPAPAPPOGSGQCVSHDCFALYPGPATFLNASQICDGLRGHLM 60
Db 1 MLGVVLGALALAGLPAPAPAPPOGSGQCVSHDCFALYPGPATFLNASQICDGLRGHLM 60
OY 61 TVRSSVADVLSLLNGDGVGRRRLWIGLQLPGCCGDPKRLGRLGRFOWTGDNNNTSYS 120
Db 61 TVRSSVADVLSLLNGDGVGRRRLWIGLQLPGCCGDPKRLGRLGRFOWTGDNNNTSYS 120
OY 121 RMARLDINGAPLCPGLCVAVSAEAATVSEPTWEEQCEVADGFLCEFHFPATCRPLAV 180
Db 121 RMARLDINGAPLCPGLCVAVSAEAATVSEPTWEEQCEVADGFLCEFHFPATCRPLAV 180
OY 181 EPGAAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGIQIMCTAPPGAVQGHMAREAP 240
Db 181 EPGAAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGIQIMCTAPPGAVQGHMAREAP 240
OY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVBNP 299
Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGRSCTASATQSCNDLCEHFCVBNP 300
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Db 301 DQPSYSQCMCTGRLADQRCCEVDVDCILBSPCPCRCVNTQSGFCHCYPNYDLVDG 360
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Db 361 ECVBPVDCFRANCEYOCOPINOTSYLCAEGFAPLPHBPHRCOMFCNOTACPADCPN 420
OY 420 TQASCECEGYILDDGFICTDIDECENGFCSGVCHNLPGTFECTICGPDALAHIGTDC 479
Db 421 TQASCECEGYILDDGFICTDIDECENGFCSGVCHNLPGTFECTICGPDALAHIGTDC 480
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Db 481 DSGKVDGDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
OY 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575
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RESULT 8

US-08-170-290A-54
Sequence 54, Application US/08170290A
Patent No. 5702931
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Morse, Michael J.
APPLICANT: Ziehlender, Laura R.
TITLE OF INVENTION: No. 5702931e1 Mitogenesis Methods and
TITLE OF INVENTION: Compositions
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-170,290A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05573

FILING DATE: 01-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/724,237
FILING DATE: 01-JUL-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 11972-58-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-170-290A-54

Query Match 98.9%; Score 3168.5; DB 1; Length 575;
Best Local Similarity 99.3%; Pred. No. 1.7e-220;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 1 MLGVVLGALALAGLPAPAPAPPOGSGQCVSHDCFALYPGPATFLNASQICDGLRGHLM 60
Db 1 MLGVVLGALALAGLPAPAPAPPOGSGQCVSHDCFALYPGPATFLNASQICDGLRGHLM 60
OY 61 TVRSSVADVLSLLNGDGVGRRRLWIGLQLPGCCGDPKRLGRLGRFOWTGDNNNTSYS 120
Db 61 TVRSSVADVLSLLNGDGVGRRRLWIGLQLPGCCGDPKRLGRLGRFOWTGDNNNTSYS 120
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Db 121 RMARLDINGAPLCPGLCVAVSAEAATVSEPTWEEQCEVADGFLCEFHFPATCRPLAV 180
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Db 301 DQPSYSQCMCTGRLADQRCCEVDVDCILBSPCPCRCVNTQSGFCHCYPNYDLVDG 360
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Db 361 ECVBPVDCFRANCEYOCOPINOTSYLCAEGFAPLPHBPHRCOMFCNOTACPADCPN 420
OY 420 TQASCECEGYILDDGFICTDIDECENGFCSGVCHNLPGTFECTICGPDALAHIGTDC 479
Db 421 TQASCECEGYILDDGFICTDIDECENGFCSGVCHNLPGTFECTICGPDALAHIGTDC 480
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OY 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575
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RESULT 9

US-08-170-290A-54
Sequence 54, Application US/08170290A
Patent No. 5256770
GENERAL INFORMATION:
APPLICANT: GLASSER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
DAVID R.
TITLE OF INVENTION: OXIDATION RESISTANT THROMBOMODULIN ANALOGS
NUMBER OF SEQUENCES: 48

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/506,325
;; FILING DATE: 09-APR-1990
;; SEQ ID NO: 7:
;; LENGTH: 572
5256770-7

Query Match 97.0%; Score 3107; DB 6; Length 572;
Best Local Similarity 98.3%; Pred. No. 4,6e-216;
Matches 565; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

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DB 298 DQPGSYSCMCESTGYRLAADQRCEDVDCCIIEPSPCPORCVNTQGGFECCHCPYNDLVDG 357
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QY 480 DSGKVDGSDSGSEPPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB 478 DSGKVDGSDSGSEPPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 537
QY 540 KKGGAARAKMEYKCAAPSKVVLQHVTRTERTPQRL 574
DB 538 KKGGAARAKMEYKCAAPSKVVLQHVTRTERTPQRL 572
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RESULT 10
US-09-509-994-2
; Sequence 2, Application US/09509994
; Patent No. 6808706
; GENERAL INFORMATION:
; APPLICANT: YUI, MASAKI
; APPLICANT: YOKOZAWA, AKIRA
; APPLICANT: MURATA, TOMOYO
; APPLICANT: TSURUTA, KAZUHISA
; APPLICANT: SHIMIZU, HIROKOTO
; TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
; TITLE OF INVENTION: SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
; FILE REFERENCE: KP-8753
; CURRENT APPLICATION NUMBER: US/09/509,994
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04609
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: JP 9-281659
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: JP 9-308523
; PRIOR FILING DATE: 1997-11-11

;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 516
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; OTHER INFORMATION: Partial amino acid sequences of a human
; OTHER INFORMATION: Thrombomodulin
US-09-509-994-2

Query Match 90.1%; Score 2885.5; DB 2; Length 516;
Best Local Similarity 99.4%; Pred. No. 3,8e-200;
Matches 513; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 1 MLGVLVIGALALAGLGPAPAPAPQPGSQCYEHDCFLALYPGPATFLNASQICDGLRGHLM 60
QY 61 TVRSSVADVLSLLNDGGVGRRLMTGLQLPGCCGDPKRLGFLRGFWTGDNNNTSYS 120
DB 61 TVRSSVADVLSLLNDGGVGRRLMTGLQLPGCCGDPKRLGFLRGFWTGDNNNTSYS 120
QY 121 RMARLDLNGAPLGGPLCVAVSAEAATVPSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLGGPLCVAVSAEAATVPSEPIWEBOCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAAVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
DB 180 EPGAAAAVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHMAREAP 240
QY 241 GAMDCSVENGGCEHCNAINPGARPCQCPAGALQADGSCCTAS--TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGGCEHCNAINPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 297
QY 300 DQPGSYSCMCESTGYRLAADQRCEDVDCCIIEPSPCPORCVNTQGGFECCHCPYNDLVDG 359
DB 301 DQPGSYSCMCESTGYRLAADQRCEDVDCCIIEPSPCPORCVNTQGGFECCHCPYNDLVDG 360
QY 360 ECVEBPVDFCFRANCEYQCOPLNQTSTYLCVCAEGFAPPIHEBHRQMFNCQTCAPADCPN 419
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DB 421 TQASCECEGYILLDGFICTDIDECENGFCGVCCHNLPGTFECICGSDSALARIHITDC 480
QY 480 DSGKVDGSDSGSEPPSPPTGSTLTTPPAVGLVHSG 515
DB 481 DSGKVDGSDSGSEPPSPPTGSTLTTPPAVGLVHSG 516
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RESULT 11
US-09-509-994-1
; Sequence 1, Application US/09509994
; Patent No. 6808706
; GENERAL INFORMATION:
; APPLICANT: YUI, MASAKI
; APPLICANT: YOKOZAWA, AKIRA
; APPLICANT: MURATA, TOMOYO
; APPLICANT: TSURUTA, KAZUHISA
; APPLICANT: SHIMIZU, HIROKOTO
; TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
; TITLE OF INVENTION: SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
; FILE REFERENCE: KP-8753
; CURRENT APPLICATION NUMBER: US/09/509,994
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04609
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: JP 9-281659
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: JP 9-308523
; PRIOR FILING DATE: 1997-11-11

NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Partial amino acid sequences of a human
US-09-509-994-1

Query Match 90.0%; Score 2881.5; DB 2; Length 516;
Best Local Similarity 99.2%; Pred. No. 7.4e-200;
Matches 512; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGPAPAPBPGSGSCVHDCFPALYPPATPLNLSQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLGPAPAPBPGSGSCVHDCFPALYPPATPLNLSQICDGLRGHLM 60
QY 61 TVRSSVADVISLILNGDGVGRRLWIGLQLPCCGDPKRLGPRGFQWVTGDNNTSYS 120
DB 61 TVRSSVADVISLILNGDGVGRRLWIGLQLPCCGDPKRLGPRGFQWVTGDNNTSYS 120
QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEQCEVXADGFLCEFHFPATCRPLAV 180
DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEQCEVXADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAAVSTTGTTPPAARQADPOLPVGSSAAVAPLGLQIMCTAPPAVQGHARAP 240
DB 181 EPGAAAAVSTTGTTPPAARQADPOLPVGSSAAVAPLGLQIMCTAPPAVQGHARAP 240
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DB 241 GAMPSCVENGCSEHACNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
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DB 300 DQPSYSCECTGYRLADQRCEDVDCCILPSPCPCRCVNTQGFECCHCYPNYDLVDG 359
QY 360 ECVRPVPCFRANCEYOCQPLNQTSTLCVCAEGFAPPIHBPBRQCMFCNQIACPADCPBN 419
DB 360 ECVRPVPCFRANCEYOCQPLNQTSTLCVCAEGFAPPIHBPBRQCMFCNQIACPADCPBN 419
QY 420 TQACECEPEGYILDDGFICTIDECENGFGSGVCHNLPGTFECICGPDALARIHIGDC 479
DB 420 TQACECEPEGYILDDGFICTIDECENGFGSGVCHNLPGTFECICGPDALARIHIGDC 479
QY 480 DSGKVDGDSGSGEPPSPPTPGSTLTPPAVGLVHSG 515
DB 480 DSGKVDGDSGSGEPPSPPTPGSTLTPPAVGLVHSG 515

RESULT 12
US-08-733-564-2
Sequence 2, Application US/08733564
Patent No. 5916874
GENERAL INFORMATION:
APPLICANT: FUJIMURA, Kenji
APPLICANT: MOCHIDA, Satoshi
TITLE OF INVENTION: METHOD FOR TREATING LIVER INJURY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/733,564
FILING DATE: 18 OCTOBER 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 0216-0362P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-733-564-2

Query Match 87.3%; Score 2795.5; DB 1; Length 498;
Best Local Similarity 99.2%; Pred. No. 1.1e-193;
Matches 494; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 19 AAPBPQSGSCVHDCFPALYPPATPLNLSQICDGLRGHLMTVRSSVADVISLILNGD 78
DB 1 AAPBPQSGSCVHDCFPALYPPATPLNLSQICDGLRGHLMTVRSSVADVISLILNGD 78
QY 79 GGVGRRLWIGLQLPCCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
DB 79 GGVGRRLWIGLQLPCCGDPKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
QY 139 AVSAEAATVSEPIWEQCEVXADGFLCEFHFPATCRPLAVEGAAAAVSTTGTTPFA 198
DB 139 AVSAEAATVSEPIWEQCEVXADGFLCEFHFPATCRPLAVEGAAAAVSTTGTTPFA 198
QY 199 ARGADPOLPVGSSAAVAPLGLQIMCTAPPAVQGHARAPGAMDCSEVNGGSEHACNA 258
DB 199 ARGADPOLPVGSSAAVAPLGLQIMCTAPPAVQGHARAPGAMDCSEVNGGSEHACNA 258
QY 259 IPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNPDPGSGSCCEFTGYRLAA 317
DB 259 IPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNPDPGSGSCCEFTGYRLAA 317
QY 318 DQRCEDVDCCILPSPCPCRCVNTQGFECCHCYPNYDLVGEVBPVPCFRANCEYOC 377
DB 318 DQRCEDVDCCILPSPCPCRCVNTQGFECCHCYPNYDLVGEVBPVPCFRANCEYOC 377
QY 361 QPLNQTSTLCVCAEGFAPPIHBPBRQCMFCNQIACPADCPDNTQASCCEPEGYILDDGFI 420
DB 361 QPLNQTSTLCVCAEGFAPPIHBPBRQCMFCNQIACPADCPDNTQASCCEPEGYILDDGFI 420
QY 438 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGDCSGKVDGDSGSGEPPSP 497
DB 438 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGDCSGKVDGDSGSGEPPSP 497
QY 481 PTPGSTLTPPAVGLVHSG 515
DB 481 PTPGSTLTPPAVGLVHSG 515

RESULT 13
US-08-312-870-3
Sequence 3, Application US/08312870
Patent No. 5639625
GENERAL INFORMATION:
APPLICANT: Carson, Craig W.
APPLICANT: Ramon, Charles T.
TITLE OF INVENTION: Method for Detecting Antibodies to
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews

STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,870
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-870-3

Query Match 87.2%; Score 2793.5; DB 1; Length 497;
Best Local Similarity 99.4%; Pred. No. 1.6e-193;
Matches 494; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 19 AAPAPGSGSCVHDECFALYGPATFLNAGQICDGLRGLMTVRSSVAADVISILLNGD 78
DB 1 AAPAPGSGSCVHDECFALYGPATFLNAGQICDGLRGLMTVRSSVAADVISILLNGD 60
QY 79 GGVGRRRLMIGLQIPPGCGDPRKLGRLGFWVTGDNNTSYSRRARLDLNGAPLCGPLCV 138
DB 61 GGVGRRRLMIGLQIPPGCGDPRKLGRLGFWVTGDNNTSYSRRARLDLNGAPLCGPLCV 120
QY 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTFFA 198
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTFFA 180
QY 199 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGSCCHACNA 258
DB 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGSCCHACNA 240
QY 259 IPGARPCCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPQGSYSCEMCTGYRLAA 317
DB 241 IPGARPCCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPQGSYSCEMCTGYRLAA 300
QY 318 DOHRCEDVDCCILBSPCPCORCVNTQGGFEGCHCYPNYDLVGECEVPEVDFRANCEYQC 377
DB 301 DOHRCEDVDCCILBSPCPCORCVNTQGGFEGCHCYPNYDLVGECEVPEVDFRANCEYQC 360
QY 378 QPLNQTSTLCVCABGFAPRPHRRCQMFNCQTACPADCDPNTQASCCEPGYIILDGFI 437
DB 361 QPLNQTSTLCVCABGFAPRPHRRCQMFNCQTACPADCDPNTQASCCEPGYIILDGFI 420
QY 438 CTDIDECENGGFCGVCCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 497
DB 421 CTDIDECENGGFCGVCCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 480
QY 498 PTPGSTLTTPPAVGLVHS 514
DB 481 PTPGSTLTTPPAVGLVHS 497

RESULT 14
US-09-331-793-4
Sequence 4, Application US/09331793

Patent No. 6500646
GENERAL INFORMATION:
APPLICANT: KURIYAMA, Shinichi
APPLICANT: HASEGAWA, Takashi
TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
FILE REFERENCE: 1110-253P
CURRENT APPLICATION NUMBER: US/09/331,793
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patent version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-331-793-4

Query Match 87.1%; Score 2789.5; DB 2; Length 497;
Best Local Similarity 99.2%; Pred. No. 3.1e-193;
Matches 493; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 19 AAPAPGSGSCVHDECFALYGPATFLNAGQICDGLRGLMTVRSSVAADVISILLNGD 78
DB 1 AAPAPGSGSCVHDECFALYGPATFLNAGQICDGLRGLMTVRSSVAADVISILLNGD 60
QY 79 GGVGRRRLMIGLQIPPGCGDPRKLGRLGFWVTGDNNTSYSRRARLDLNGAPLCGPLCV 138
DB 61 GGVGRRRLMIGLQIPPGCGDPRKLGRLGFWVTGDNNTSYSRRARLDLNGAPLCGPLCV 120
QY 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTFFA 198
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTFFA 180
QY 199 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGSCCHACNA 258
DB 181 ARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGSCCHACNA 240
QY 259 IPGARPCCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPQGSYSCEMCTGYRLAA 317
DB 241 IPGARPCCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPQGSYSCEMCTGYRLAA 300
QY 318 DOHRCEDVDCCILBSPCPCORCVNTQGGFEGCHCYPNYDLVGECEVPEVDFRANCEYQC 377
DB 301 DOHRCEDVDCCILBSPCPCORCVNTQGGFEGCHCYPNYDLVGECEVPEVDFRANCEYQC 360
QY 378 QPLNQTSTLCVCABGFAPRPHRRCQMFNCQTACPADCDPNTQASCCEPGYIILDGFI 437
DB 361 QPLNQTSTLCVCABGFAPRPHRRCQMFNCQTACPADCDPNTQASCCEPGYIILDGFI 420
QY 438 CTDIDECENGGFCGVCCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 497
DB 421 CTDIDECENGGFCGVCCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 480
QY 498 PTPGSTLTTPPAVGLVHS 514
DB 481 PTPGSTLTTPPAVGLVHS 497

RESULT 15
US-08-014-723-14
Sequence 14, Application US/08014723
Patent No. 5273962
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saito, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Okuchi, Maeko
TITLE OF INVENTION: Thrombin-Binding Substance and Process
NUMBER OF SEQUENCES: 18
CORESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-014-723-14

Query Match 85.4%; Score 2735.5; DB 1; Length 494;
Best Local Similarity 98.6%; Pred. No. 2.4e-189;
Matches 487; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 MLGVIVLALALAGFPAPAPPOGSGCVCHDPCALYRGPATFLNASQICDGLRGLHM 60
DB 1 MLGVIVLALALAGFPAPAPPOGSGCVCHDPCALYRGPATFLNASQICDGLRGLHM 60
QY 61 TVRSSVADVISLNLNGDGVGRRLMIGLOLPPCGDPRKRLGPIRGFOWVTGDNNTSYS 120
DB 61 TVRSSVADVISLNLNGDGVGRRLMIGLOLPPCGDPRKRLGPIRGFOWVTGDNNTSYS 120
QY 121 RWARIDINGAPLCGPLCAVSAABATVPSEPIWBEQCEVKADGFLCEHFEPATCRPLAV 180
DB 121 RWARIDINGAPLCGPLCAVSAABATVPSEPIWBEQCEVKADGFLCEHFEPATCRPLAV 180
QY 181 EPGAAAASVTYGTFFPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
DB 181 EPGAAAASVTYGTFFPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
QY 241 GAMDCSVENGCEHCNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGCEHCNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVNP 299
QY 300 DQPGSYSCMCEGTGYRLADQHRCEVDVDCILPSPFCPCVNTQGGFECHCYPNYDLVYG 359
DB 300 DQPGSYSCMCEGTGYRLADQHRCEVDVDCILPSPFCPCVNTQGGFECHCYPNYDLVYG 359
QY 360 ECVFVVDPCFRANCYOCQPLNQTSTLYCYCAEGFAPIPHEPRCOMFCNQTRACPADCDPN 419
DB 360 ECVFVVDPCFRANCYOCQPLNQTSTLYCYCAEGFAPIPHEPRCOMFCNQTRACPADCDPN 419
QY 420 TQASCECEPEGYILDDGFICTDIDECENGFGSGVCCHNLPGTFPECICGPDALVRHIGTDC 479
DB 420 TQASCECEPEGYILDDGFICTDIDECENGFGSGVCCHNLPGTFPECICGPDALVRHIGTDC 479
QY 480 DSGKVDGDSGSGE 493
DB 480 DSGKVDGDSGSGE 493

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:24:42 ; Search time 246 Seconds

(without alignments)
1646.233 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203

Sequence: 1 MLGVLVIGALALAGLPPAP.....APSKKVLQHVTRTERTPQRL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	575	1 TRBM_HUMAN	P07204 homo sapien
2	3176.5	99.2	575	1 TRBM_SALIC	Q71U07 salmifl sci
3	3172.5	99.0	575	2 O81V29_HUMAN	O81V29 homo sapien
4	2317	72.3	578	1 TRBM_CANFA	O5W7P8 canis famli
5	2236	69.8	580	2 Q8H248_RABIT	Q8H248 oryctolagus
6	2113.5	66.0	577	1 TRBM_MOUSE	P15306 mus musculu
7	2113.5	66.0	577	1 TRBM_MOUSE	O543W3 mus musculu
8	2046.5	63.9	577	2 O8HJ85_MOUSE	O8HJ85 mus musculu
9	1799	56.2	491	2 O8HJ85_MOUSE	P97883 rattus norv
10	1600	50.0	461	2 TRBM_BOVIN	P06579 bos taurus
11	1314	41.0	356	1 TRBM_BOVIN	Q4WS22 tetradon n
12	651.5	20.3	496	2 Q4WS22_TETNG	Q4WS22 tetradon n
13	604.5	18.9	431	2 Q4WS22_TETNG	Q4WS22 tetradon n
14	597	18.6	431	2 Q4WS22_TETNG	Q4WS22 tetradon n
15	590.5	18.4	652	1 C10R1_HUMAN	O9N9Y3 homo sapien
16	586.5	18.3	652	1 C10R1_HUMAN	O81XK1 homo sapien
17	585	18.3	606	2 Q544N0_XENTIA	O544N0 xenopus lae
18	578	18.0	757	2 O9HCU0_HUMAN	O9HCU0 homo sapien
19	575	18.0	765	2 O9HCU0_HUMAN	O9HCU0 homo sapien
20	575	18.0	765	2 O9HCU0_HUMAN	O9HCU0 homo sapien
21	546	17.0	512	2 O4SMV1_TETNG	O4SMV1 mus musculu
22	545	17.0	512	2 O4SMV1_TETNG	O4SMV1 mus musculu
23	531	16.6	643	1 C10R1_MOUSE	O89103 mus musculu
24	529.5	16.5	589	2 Q4R1P1_RAT	Q4R1P1 rattus norv
25	481	15.0	136	2 Q792T4_RAT	Q792T4 rattus norv
26	426	13.3	1664	2 O9TVQ2_CABERL	O9TVQ2 caenorhabdi
27	414.5	12.9	1574	1 EGFL3_RAT	O88281 rattus norv
28	409.5	12.8	1277	2 Q7PFC0_ANOGA	Q7PFC0 anopheles g
29	398.5	12.4	1168	2 O6XCO_CABBR	O6XCO caenorhabdi
30	391	12.2	708	2 P87363_CHICK	P87363 gallus galli
31	386.5	12.1	1577	2 Q9V889_DROME	Q9V889 drosophila

32	384	12.0	2871	1 FBNI_BOVIN	P98133 bos taurus
33	384	12.0	2871	1 FBNI_HUMAN	P35555 homo sapien
34	384	12.0	2871	1 FBNI_PIG	O9CV36 sus scrofa
35	384	12.0	2871	2 O75N87_HUMAN	O75N87 homo sapien
36	384	12.0	3857	2 O88840_MOUSE	O88840 mus musculu
37	382	11.9	2871	1 FBNI_MOUSE	O61554 mus musculu
38	381.5	11.9	2225	2 Q571J3_MOUSE	O571J3 mus musculu
39	378	11.8	1362	2 Q559U0_DICDI	O559U0 dictyosteli
40	378	11.8	2884	2 Q4SHN1_TETNG	Q4SHN1 tetradon n
41	377.5	11.8	941	2 O54YPO_DICDI	O54YPO dictyosteli
42	377	11.8	2872	2 O9WH9_RAT	O9WH9 rattus norv
43	376.5	11.8	2906	2 Q9WH9_RAT	O9WH9 rattus norv
44	374.5	11.7	2907	1 FBNI_MOUSE	O61555 mus musculu
45	373.5	11.7	1976	2 Q595S6_HUMAN	Q595S6 homo sapien

ALIGNMENTS

RESULT 1

ID	TRBM_HUMAN	STANDARD	PRT	575 AA.
AC	P07204; Q9UC32;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Thrombomodulin precursor (TM) (Fetomodulin) (CD141 antigen).			
GN	Name=THBD; Synonyms=THRM;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 19-43.			
RX	MEDLINE=8604395; PubMed=2820710;			
RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioka J., Maruyama I.,			
RA	Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;			
RT	"Structure and expression of human thrombomodulin, a thrombin receptor on endothelium acting as a cofactor for protein C activation.";			
RT	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RX	MEDLINE=86024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;			
RT	"Human thrombomodulin: complete cDNA sequence and chromosome localization of the gene.";			
RT	localization of the gene.";			
RT	biochemistry 26:4350-4357(1987).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=87317665; PubMed=2819876;			
RA	Jackman R.W., Beeler D.L., Fritze L., Soff G., Rosenberg R.D.;			
RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDNA and gene predict protein structure and suggest sites of regulatory control.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=86227901; PubMed=2836377;			
RA	Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.;			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activation of protein C.";			
RT	J. Biochem. 103:281-285(1988).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT VAL-473.			
RA	Rider M.J., Armet T.Z., Carlington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toch E.J., Yi Q., Nickerson D.A.;			
RT	"Sequences, NHBI H16682 program for genomic applications, UM-			
RT	PHRCR, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RT	Submitted (MMR-2002) to the EMBL/Genbank/DBJ databases.			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			

RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA DeJoukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S.V., Cobley V.E., Collier R.E., Connor R.E., Coby N.R.,
 RA Coulson A., Coville G.J., Deaman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafton D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kip M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Kshirsagar M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA March V.L., Martin S.L., McConachie L.J., McElay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K.A., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showmken R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulterson J.B.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [7]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadit T.B., Toshiyuki S., Carinini P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RN CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
 RP MEDLINE=94029900; PubMed=8216207;
 RX Gerlitz B., Hasegall T., Vlahos C.J., Parkinson J.F., Bang N.U.,
 RA Grinnell B.W.;
 RT "Identification of the predominant glycosaminoglycan-attachment site
 RT in soluble recombinant human thrombomodulin: potential regulation of
 RT functionality by glycosyltransferase competition for serine 474.";
 RL Biochem. J. 295:131-140(1993).
 [9]
 RN HYDROXYLATION OF ASN-342.
 RP MEDLINE=93293792; PubMed=8390446;
 RX Yamamoto S., Mizoguchi T., Tamaki T., Okuchi M., Kimura S., Aoki N.;
 RT "Urinary thrombomodulin, its isolation and characterization.";
 RL J. Biochem. 113:433-440(1993).
 [10]
 RN STRUCTURE BY NMR OF 389-407.
 RP MEDLINE=96007474; PubMed=7559494; DOI=10.1074/jbc.270.40.23366;
 RX Adler M., Seto W.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;
 RT "The structure of a 19-residue fragment from the C-loop of the fourth
 RT epidermal growth factor-like domain of thrombomodulin.";
 RL J. Biol. Chem. 270:23366-23372(1995).
 [11]
 RN STRUCTURE BY NMR OF 364-407.
 RP MEDLINE=96100636; PubMed=8528067;
 RX Meininger D.P., Hunter M.J., Komives E.A.;
 RT "Synthesis, activity, and preliminary structure of the fourth EGF-like
 RT domain of thrombomodulin.";
 RL Protein Sci. 4:1683-1695(1995).
 [12]
 RN STRUCTURE BY NMR OF 427-444.
 RP MEDLINE=95034791; PubMed=7947766;
 RX Srinivasan U., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
 RT "Thrombin-bound structure of an EGF subdomain from human
 RT thrombomodulin determined by transferred nuclear Overhauser effects.";
 RL Biochemistry 33:13553-13560(1994).
 [13]
 RN STRUCTURE BY NMR OF 427-444.
 RP MEDLINE=96276211; PubMed=8745396;
 RX Hrabal R., Komives E.A., Ni F.;
 RT "Structural resiliency of an EGF-like subdomain bound to its target
 RT protein, thrombin.";
 RL Protein Sci. 5:195-203(1996).
 [14]
 RN STRUCTURE BY NMR OF 405-444.
 RP MEDLINE=98035729; PubMed=9367781; DOI=10.1006/jmbi.1997.1356;
 RX Sampaio Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;
 RT "Structure of the fifth EGF-like domain of thrombomodulin: an EGF-like
 RT domain with a novel disulfide-bonding pattern.";
 RL J. Mol. Biol. 273:913-926(1997).
 [15]
 RN VARIANT TED TYR-486.
 RP MEDLINE=9511115; PubMed=7811989;
 RX Oehlin A.-K., Marlar R.A.;
 RT "The first mutation identified in the thrombomodulin gene in a 45-
 RT year-old man presenting with thromboembolic disease.";
 RL Blood 85:330-336(1995).
 [16]
 RN VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.
 RP MEDLINE=97341986; PubMed=9198186;
 RX Oehlin A.-K., Norlund L., Marlar R.A.;
 RT "Thrombomodulin gene variations and thromboembolic disease.";
 RL Thromb. Haemost. 78:396-400(1997).
 [17]
 RN VARIANT VAL-473.
 RP MEDLINE=97206518; PubMed=9157575;
 RX Norlund L., Holm J., Zoller B., Oehlin A.-K.;
 RT "A common thrombomodulin amino acid dimorphism is associated with
 RT myocardial infarction.";
 RL Thromb. Haemost. 77:248-251(1997).
 [18]
 RN VARIANT THR-43.
 RP MEDLINE=99057299; PubMed=9843165;
 RX Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
 RA Stubbé P.J., Manger Cate V., Ireland H.;
 RT "A mutation in the thrombomodulin gene, 127G to A coding for Ala25thr,
 RT and the risk of myocardial infarction in men.";
 RL Thromb. Haemost. 80:743-748(1998).
 [19]
 RN VARIANT VAL-473.
 RP MEDLINE=21143723; PubMed=11245641;
 RX Wu K.K., Alekic N., Ann C., Boerwinkle E., Folsom A.R., Juneja H.;
 RT "Thrombomodulin Ala45Val polymorphism and risk of coronary heart
 RT disease.";
 RL Circulation 103:1386-1389(2001).
 [20]
 RN VARIANT TED TYR-486, AND VARIANT VAL-473.
 RP MEDLINE=22135346; PubMed=12139752;
 RX DOI=10.1046/j.1365-2141.2002.03644.x;
 RA Falout E.M., Franchi F., Castaman G., Biguzzi E., Rodeghiero F.;
 RT "Mutations in the thrombomodulin gene are rare in patients with severe
 RT thrombophilia.";
 RL Br. J. Haematol. 118:595-599(2002).
 CC -!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor

Query Match	99.2%	Score 3176.5	DB 1	Length 575
Best Local Similarity	99.5%	Pred 70.2e-202		
Matches	572	Conservative	0	Mismatches 2; Indels 1; Gaps 1
CC	that forms a 1:1 stoichiometric complex with thrombin. This complex is responsible for the conversion of protein C to the			
CC				
QY	1	MLGVLVLTALALAGLPAPAPPOGGSCVHDCFPALPGPATFLNLSQICDGLRHLM	60	
Db	1	MLGVLVLTALALAGLPAPAPPOGGSCVHDCFPALPGPATFLNLSQICDGLRHLM	60	
QY	61	TVRSSVAADVLSLLINGDGGVGRRLMTGLQLPCCGGDPKRLGLPLRGFOWTGDNNNTSYS	120	
Db	61	TVRSSVAADVLSLLINGDGGVGRRLMTGLQLPCCGGDPKRLGLPLRGFOWTGDNNNTSYS	120	
QY	121	FWARLDLNGAPLCGLPVAVSAAEKTVBEPITWEEQCEVKADGFLCEHPFATPRPLAV	180	
Db	121	FWARLDLNGAPLCGLPVAVSAAEKTVBEPITWEEQCEVKADGFLCEHPFATPRPLAV	180	
QY	181	EPGAAAAAVSITVGFPPAPAGDPALPVGGSAVAAPLGLQLMCTAPPGA VOGHAREAP	240	
Db	181	EPGAAAAAVSITVGFPPAPAGDPALPVGGSAVAAPLGLQLMCTAPPGA VOGHAREAP	240	
QY	241	GAMDCSVENGCEHA CNM1 PGARPCQCPAGALQADGSSCTASATQSCNDLCEHF CVNPP	299	
Db	241	GAMDCSVENGCEHA CNM1 PGARPCQCPAGALQADGSSCTASATQSCNDLCEHF CVNPP	299	
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DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Thrombomodulin precursor (TM).			
GN	Name=THBD; Synonyms=TMSC;			
OS	Salutari scuturus (Common squirrel monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;			
OC	Cebinae; Salitri.			
OX	NCBI_TaxID=9521;			
RP	NUCLEOTIDE SEQUENCE.			
RA	Parry D., Fuesi T., Torrentino M., Pouvelle B., Gysin J.;			
RT	"Salutari scuturus thrombomodulin gene."			
RL	Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.			
CC	-!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor			
CC	that forms a 1:1 stoichiometric complex with thrombin. This			
CC	complex is responsible for the conversion of protein C to the			
CC	activated protein C (protein Ca). Once evolved, protein Ca			
CC	activations the activated cofactors of the coagulation mechanism,			
CC	factor Va and factor VIIIa, and thereby reduces the amount of			

CC		thrombin generated (By similarity).
CC	-1-	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1-PTM:	N-glycosylated (By similarity).
CC	-1-	SIMILARITY: Contains 1 C-type lectin domain.
CC	-1-	SIMILARITY: Contains 6 EGF-like domains.
CC		-----
CC		This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC		-----
DR	EMBL:	AF169484; AAD49735.1; - Genomic DNA.
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DR	InterPro:	IPIR000742; EGF_2.
DR	InterPro:	IPIR001881; EGF_Ca bd.
DR	InterPro:	IPIR006209; EGF_Like.
DR	InterPro:	IPIR006210; IEFG.
DR	InterPro:	IPIR001304; Lectin_C.
DR	InterPro:	IPIR001491; Thrombomodulin.
DR	Pfam:	PF00008; EGF_2.
DR	Pfam:	PF07645; EGF_CA; 2.
DR	Pfam:	PF00059; Lectin_C; 1.
DR	PRINTS:	PRO0907; THROMBOMODULN.
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DR	SMART:	SMO0181; EGF; 6.
DR	SMART:	SMO0179; EGF_CA; 4.
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DR	PROSITE:	PS01186; EGF_2; 2.
DR	PROSITE:	PS50026; EGF_3; 4.
DR	PROSITE:	PS01187; EGF_CA; 2.
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FT DISUFID 451 464 By similarity.
 FT DISUFID 466 480 By similarity.
 SQ SEQUENCE 575 AA; 60329 MW; 9AF03CD151227D52 CRC64;
 Query Match 99.2%; Score 3176.5; DB 1; Length 575;
 Best Local Similarity 99.5%; Pred. No. 7.2e-202;
 Matches 571; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MLGVLVIGALALAGLPAPAPAPPGSGSQCYEHDCFLPYGPATFLNLSQICDGLRGLM 60
 DB 1 MLGVLVIGALALAGLPAPAPAPPGSGSQCYEHDCFLPYGPATFLNLSQICDGLRGLM 60
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 QY 121 RMARLDINGAPLCPPLCVAVSAEAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
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 DB 541 KKGGAARAKMEYKCAASKEVVLQHVTERTPORL 575
 RESULT 3
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 ID Q8IV29
 AC Q8IV29
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Thrombomodulin.
 GN Name:THBD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chariotontogliares; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_Taxid=9606;
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 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Martuna K., Farmer A.A., Kudin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.T., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toohyuki S., Garinaci P., Prange C.,
 RA Rana S.S., Loguallino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
 RA Schencher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RG NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC035602; AAH35602.2; -, mRNA.
 DR HSSP; P07204; 12AQ.
 DR Ensembl; ENSG00000178726; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR InterPro; IPR000152; Aex_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF07645; EGF; 2.
 DR Pfam; PF00059; Lectin_C; 1.
 DR PRINTS; PR00307; THROMBOMODULN.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 6.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 2.
 SQ SEQUENCE 575 AA; 60357 MW; 9252B6F9E01963AC CRC64;
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1.3e-201;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MLGVLVIGALALAGLPAPAPAPPGSGSQCYEHDCFLPYGPATFLNLSQICDGLRGLM 60
 DB 1 MLGVLVIGALALAGLPAPAPAPPGSGSQCYEHDCFLPYGPATFLNLSQICDGLRGLM 60
 QY 61 TVRSSVADYVSLILNDGCVGRRRLWIGQLPPGCCDPRKGLRGRFOWTGNNTSYS 120
 DB 61 TVRSSVADYVSLILNDGCVGRRRLWIGQLPPGCCDPRKGLRGRFOWTGNNTSYS 120
 QY 121 RMARLDINGAPLCPPLCVAVSAEAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 DB 121 RMARLDINGAPLCPPLCVAVSAEAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 DB 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
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 DB 241 GAMDCSYENGSCHEACNAIPGAPRCQCPAGALQADRSCTASATQSCNDLCHEFCVNP 300
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Db 541 KKGARARAMEYKCAAPSKEVVLQHVTRTERPQRL 575

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RESULT 4

TRBM_CANPA STANDARD; PRT; 578 AA.

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ID TRBM_CANPA STANDARD; PRT; 578 AA.
AC QSW7B8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thrombomodulin precursor (TM).
GN Name=THBD;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
OX [1]
RX NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX PubMed:15585960;
RA Maruyama H., Ogura K., Maeda S., Kano R., Teujimoto H., Watari T.,
RA Tokuriki M., Hasegawa A.;
RT "Molecular cloning of canine thrombomodulin cDNA and expression in
RT normal tissues."
RL J. Vet. Med. Sci. 66:1423-1427(2004).
CC -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
CC that forms a 1:1 stoichiometric complex with thrombin. This
CC complex is responsible for the conversion of protein C to the
CC activated protein C (protein Ca). Once evolved, protein Ca
CC ectases the activated cofactors of the coagulation mechanism,
CC factor Va and factor VIIIa, and thereby reduces the amount of
CC thrombin generated (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in lung, liver, spleen, kidney,
CC pancreas and lymph node. Low expression in heart, cerebrum,
CC urinary bladder and uterus.
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Contains 1 C-type lectin domain.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB193481; BAD6823.1.-; mRNA.
DR InterPro; IPR000152; AaX_Hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001491; ThrmDomModuln.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF07645; EGF_CA; 1.

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DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00907; THRMOMODULN.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR Blood coagulation; EGF-like domain; Glycoprotein; Hydroxylation;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 17 578
FT TOPO_DOM 17 518
FT TRANSMEM 519 539
FT TOPO_DOM 540 578
FT DOMAIN 31 167
FT DOMAIN 242 282
FT DOMAIN 285 325
FT DOMAIN 326 364
FT DOMAIN 366 406
FT DOMAIN 405 441
FT DOMAIN 442 481
FT MOD_RES 343 343
FT CARBOHYD 114 114
FT CARBOHYD 300 300
FT CARBOHYD 410 410
FT CARBOHYD 493 493
FT CARBOHYD 495 495
FT DISULFID 246 257
FT DISULFID 253 266
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FT DISULFID 428 440
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FT DISULFID 466 480
SQ SEQUENCE 578 AA; 60745 MW; 06D255C9B8FCC083 CRC64;

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Query Match 72.3%; Score 2317; DB 1; Length 578;
 Best Local Similarity 73.2%; Pred. No. 4,9e-145;
 Matches 426; Conservative 44; Mismatches 100; Indels 12; Gaps 8;

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Oy 1 MGVTVVIGALALAGIGPPAPAPPPGSGSCYEHDCFPALYPGPATFLNASQICDGLRHLM 60
Db 1 MLRVTLIGVLAIPAGIGLPTPAQPPRSSQCEHDCFOLEFRGPATFLAASQTCCEGIGHLM 60
Oy 61 TVRSSVADVATSLILNDGGVGRRLWTGLQTPPGCGDPKRLGLRGQWYTGNNNSYS 120
Db 61 TVRSSVADVATSLILNDGGVGRRLWTGLQTPPGCGDPKRLGLRGQWYTGNNNSYS 119
Oy 121 RWARLDLNGA-PLCGPLCAVAVSAEAATVPSPIWEBOCEVAKADGFLCEFFHPATCRPIA 179
Db 120 RWARPHVGPAPPCAPLCVANSDDAAAPAPGSPNABEGRCAEAADGFLCEFFHPASCRPL 179
Oy 180 VEPGAAAA-VSTYTGPPPARAGADFOALPYGSSAAVAAPGLQLMCTAPPAVQGHMARE 238
Db 180 VDAARAAAAAGVSTYTPFGARAGADFOALPYGSSAAVAAPFGVQLACAPRGEAEARWGRE 239

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RESULT 5		
AC	QBHZ48_RABIT	
ID	QBHZ48_RABIT PRELIMINARY;	PRT; 580 AA.
AC	QBHZ48;	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DE	Thrombomodulin precursor.	
GN	Name=Thbd;	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae	
OC	Oryctolagus.	
OX	NCBI_TaxId=9986;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RP	PubMed=15016348; DOI=10.1080/10425170310001608416;	
RA	Denina C.B., Kim A.Y., Bian C.E., Regard J.B., Rade J.J.;	
RT	cDNA cloning of rabbit thrombomodulin and characterization of gene	
RT	expression in cardiovascular tissue.";	
RL	DNA Seq. 14:399-405(2003).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RA	Denina C.B., Kim A.Y., Rade J.J.;	
RT	"Cloning of rabbit thrombomodulin cDNA sequence.";	
RT	Submitted (MAR-2003) to the EMBL/Genbank/DBD databases.	
RN	[3]	
RP	PROTEIN SEQUENCE.	
RP	PubMed=2536746;	
RA	Stearns D.J., Kurosawa S., Emon C.T.;	
RT	"Microthrombomodulin. Residues 310-486 from the epidermal growth	
RT	factor precursor homology domain of thrombomodulin will accelerate	
RT	protein C activation.";	
RL	J. Biol. Chem. 264:3352-3356(1989).	
DR	EMBL; AY138902; AAN15931.2; -; mRNA.	
DR	PIR; A33308; A33308.	
DR	HSSP; P07204; 1TMR.	
DR	SMR; QBHZ48; 364-479.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0005509; F:calcium ion binding; IEA.	
DR	GO; GO:0005529; F:sugar binding; IEA.	
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.	
DR	GO; GO:0007596; P:blood coagulation; IEA.	
DR	InterPro; IPR000152; Asx_hydroxyl_S.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR006209; EGF like.	
DR	InterPro; IPR001304; Lectin C.	

Query	Match	Similarity	69.8%	Score 2236	DB 2	Length 580
InterPro: IPR002919, Prot Inh CR TIL.	InterPro: IPR001491, Thrombomodulin.					
DR pfam: PF00008; EGF_2.	DR pfam: PF07645; EGF_CA_1.					
DR pfam: PF00059; Lectin C_1.	DR PRINTS; PRO0907; THROMBOMODULIN.					
DR SMART; SMO0034; CLECT_1.	DR SMART; SMO0179; EGF_CA_1.					
DR PROSITE; PS00010; ASX_HYDROXYL_2.	DR PROSITE; PS00041; C_Type_Lectin_2_1.					
DR PROSITE; PS01186; EGF_2_3.	DR PROSITE; PS00026; EGF_3_3.					
DR PROSITE; PS01187; EGF_CA_2.	Signal.					
FT SIGNAL.	1	19	Potential.			
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Query Match	69.8%	Score 2236	DB 2	Length 580		
Best local similarity	72.0%	Pred. No. 1,1e-139				
Matches 417;	Conservative 35;	Mismatches 107;	Indels 20;	Gaps 9		
4	VLVIGATLALAGIGFAPAPAPPGSGSQCEVHDCFALYPGPATFLNLSQICDGLGHLMTVR	63				
6	ILLIGALAPAGIGLPTHAEPQDSQCEVHDCFALFRGPATFLAAGTCERCGHLMTVR	65				
64	SSVADVLSLLINGDGVGRRLMTGLDPGCCDPKRLGLPRGOWTGNNTSYSRA	123				
66	SSVADVLSLLISDSDS---PRLMTGLDLPFGCSHPGLRPRGFQWTDNRITSRA	121				
124	RLDINGAPLGCPLCYAVALAAEATVSEPIWEESQCEVADGFLCEFHNPATCRPLAVEBG	183				
122	RQDGGAPAVCCPLCYTVASAAABGEFAMEBELPGTEVDGLCEFPFAASCRPLLVEAG	181				
184	AAAAA---VSITTYGTPFAAGADFGALPVSSAAVAPLGLQMTAPPGAVOGHMAREAP	240				
182	AAPATAPVSVSTYSPFGARGADFGALPVGSSAAVAPLGLTLTCYAPGAAEAFWGREAP	241				
241	GAMDCSVENGCEHAACNAPGARPCQCGAALQADGSSCT-ASTQSCNDLCEHRCVNP	299				
242	GAMDCSVNGGCEFPACNNSAGAPRLCLCPDGAAPQADGSCAPAAPPSCHDLCEHRCVNTS	301				
300	DQPGSYSCMCEGYRLADQRCCEVDVDCILESPSPORCVNTQSGFECHCYPNYDLVDG	359				
302	DASGYSYCMCEGYRLVADGHCCEVDVDCALVPNCPQLCVNTQSGFECHCYPNYDLVDG	361				
360	ECVEBVDCEFRANCEYQCPLNOTSYLTCVCAEGFAPRPHBPRHRCMFCNQTCAPADCPN	419				
362	ECVEBVDCEFCGNCYQCLPLQGYRRLTCAGFAPVDEBPRHRCMFCNQTCAPADCPN	420				
420	TQASCECEGYILLDDGFLCTDIDECENGAFCSGVCHNLPGTFECICGPDALARIHGTDC	479				
421	YPTCTLCPREGYILLDEGSLCADIDECND-GYCDDECRNLPGSYECICGPDPSPLAGVSTEC	479				
480	-----DSGRYDGG-DSSGSGPRPPTGSTR-LTPPAVLVHSGLLIGSTINSLCLVAL	531				
480	YPTQVSDGG--DGGDGGSGEPGSGAGSPTAPPAAGPVHSGVALINSTSLVAL	537				
532	LALCLHRLKKGAAAKMEYKCAAPSKSVYLQHVTEET	570				
538	LALCLHRLKKGSGAHEFYKCAAPKAVVLQVATEET	576				

OC Mammalia; Euteria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=89128454; PubMed=2536925;
 RA Dittman W.A., Majerus P.W.;
 RT "Sequence of a cDNA for mouse thrombomodulin and comparison of the
 RT predicted mouse and human amino acid sequences.";
 RL Nucleic Acids Res. 17:802-802(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89008498; PubMed=2844823;
 RA Dittman W.A., Kumada T., Sadler J.E., Majerus P.W.;
 RT "The structure and function of mouse thrombomodulin. Phorbol myristate
 RT acetate stimulates degradation and synthesis of thrombomodulin without
 RT affecting mRNA levels in hemangioma cells.";
 RL J. Biol. Chem. 263:15815-15822(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
 CC that forms a 1:1 stoichiometric complex with thrombin. This
 CC complex is responsible for the conversion of protein C to the
 CC activated protein C (protein C). Once evolved, protein C to the
 CC activates the activated cofactors of the coagulation mechanism,
 CC factor Va and factor VIII, and thereby reduces the amount of
 CC thrombin generated.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
 CC thrombomodulin (By similarity).
 CC -1- SIMILARITY: Contains 1 C-type lectin domain.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: X14432; CAAG2597.1; -; mRNA.
 DR EMBL: BC019154; AAH19154.1; -; mRNA.
 DR PIR: S08488; A60501.
 DR HSP: P07204; 1BGT.
 DR MGI: MGI:98736; Thbd.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005886; C:plasma membrane; TAS.
 DR GO: GO:0007596; P:blood coagulation; TAS.
 DR GO: GO:0009790; P:embryonic development; IMP.
 DR GO: GO:0050819; P:negative regulation of coagulation; TAS.
 DR GO: GO:0007565; P:pregnancy; IMP.

DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF07645; EGF_Ca_1.
 DR Pfam; PF00059; Lectin_C_1.
 DR PRINTS: PR00907; THROMBOMODULIN.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA_1.
 DR PROSITE; PS00010; ASX_HYDROXYL_2.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA_2.
 KW Blood coagulation; EGF-like domain; Glycoprotein; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 1 577
 FT TOPO_DOM 17 517
 FT TRANSMEM 518 541
 FT TOPO_DOM 542 577
 FT DOMAIN 31 167
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 FT DOMAIN 283 323
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 DB 1 MLGLFPLGVLPAVALGSLAKLQPTGSCVCEHCPLFPQAPVFLDASQACQRLQGHLM 60
 QY 61 TVRSSVADYVILSLINGDG-GVGRRLWTIGLPLPGCGDPRRLGLPLRGFQWVTGDNNTSY 119
 DB 61 TVRSSVADYVILSLSSNDLGP---WIGLQLPQCGDDPRHLGLPLGFGQWVTGDNNTSY 117
 QY 120 SRWAPLDLNGAPLCGPLCVAVSAAEATVPSEPIWEEOCCVAKDGLCEFPATCPPLA 179
 DB 118 SRWAPLDQFAPLCPGLCVTVSTATEAAPGEPAWEERKCEETETGFLCEFYFTASCRPLT 177

QY 180 VEP-GAAAAVSTYGTFFARAGDFQRLPVGSSAAVAPLQIMCTAPGAVOGHWARE 238
 DB 178 VNRDPEAAHHSSTYNTPEVGSADFQRLPVGSSAAVAPLQIMCTAPGAVOGHWAME 237
 QY 239 APGAMDCSVENGCEHACNAIPGARPCCCPAGAAALQADGSCCTAS-TGSCNDLCEHFVCP 297
 DB 238 ATGAMNCSVENGCCEYLGNRSTNEPRCLCPRMDLQADGRSCAPPVVSGCNELCEHFVCS 297
 QY 298 NPDPGSGVSCMCEGYRLAADOHCEVDDCILIEBSPCPCQVMTQGGFECHCQPNYDLY 357
 DB 298 NAEVPGSISCMCEGYRLAADOHCEVDDCILIEBSPCPCQVMTQGGFECHCQPNYDLY 357
 QY 358 DGECEVPCPCFRANACEYQCCPLNQTSTLCVCAEGFAPRPHRQCMQCNQACPADCD 417
 DB 358 DGECEVPCPCFRANACEYQCCPLNQTSTLCVCAEGFAPRPHRQCMQCNQACPADCD 417
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 DB 418 PNTQASCCEPGYLLIDGFCITDIDECNNGFCSCGVCHNLRTGTEPCTCGPSSALARIHGT 477
 QY 478 DCDSDGK---DGGDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASICLVVALLAL 534
 DB 478 DCDSDGK---DGGDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASICLVVALLAL 534
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 DB 535 LCHLRKQGAARAKMEYKCAAPSKVEVLAQHRTERTPOR 573
 QY 573 LCHLRKQGAARAKMEYKCAAPSKVEVLAQHRTERTPOR 573
 DB 573 LCHLRKQGAARAKMEYKCAAPSKVEVLAQHRTERTPOR 573
 RESULT 7
 ID 0543W3_MOUSE PRELIMINARY; PRT; 577 AA.
 AC 0543W3_MOUSE PRELIMINARY; PRT; 577 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched
 DE library, clone: B130014A08 product: THROMBOMODULIN (PETOMODULIN) (TM),
 DE full insert sequence (Thbd protein).
 GN Name=Thbd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kanai A., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochi H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Steubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guerinich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Norioka F., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,

RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kanaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki R., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanaji A., Matsuda H., Batalov S., Beisler K.W.,
 RA Blake J., Brad T., Brusio V., Chochla C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glass C., Godzik A., Gough J.,
 RA Grimmond S., Guerinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kanaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petter G., Pesole G.,
 RA Petrovsky N., Piliat R., Pontius J.V., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempere C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszew-Boris A., Yanagisawa M., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuana T., Teshiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsumoto T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.,
 RT "Cloning of mouse full open reading frames in Gateway(R) system entry
 vector (pDONR201)."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AK044928; BAC32146.1; -; mRNA.
 DR EMBL, CT010375; CBJ18582.1; -; mRNA.
 DR MGI, MGI:98735; Thbd.
 DR GO, GO:0005615; C:extracellular space; TAS.
 DR GO, GO:0016021; C:integral to membrane; TAS.
 DR GO, GO:0005866; C:plasma membrane; TAS.
 DR GO, GO:0007966; P:blood coagulation; TAS.
 DR GO, GO:0009790; P:embryonic development; IMP.
 DR GO, GO:0050819; P:negative regulation of coagulation; TAS.
 DR GO, GO:0007565; P:pregnancy; IMP.
 DR InterPro, IPR000152; Asx_hydroxyl_5.
 DR InterPro, IPR000742; EGF_2.
 DR InterPro, IPR001881; EGF CA. bd.
 DR InterPro, IPR006209; EGF-like.
 DR InterPro, IPR006210; IEGF.
 DR InterPro, IPR001304; Lectin C.
 DR InterPro, IPR001491; Thrombomodulin.
 DR Pfam, PF00008; EGF_1.
 DR Pfam, PF07645; EGF CA; 1.
 DR Pfam, PF00059; Lectin C; 1.
 DR PRINTS, PR00907; THROMMODULN.
 DR SMART, SM00034; CLECT; 1.
 DR SMART, SM00181; EGF; 6.
 DR SMART, SM00179; EGF CA; 4.
 DR PROSITE, PS00010; ASX_HYDROXYL; 2.
 DR PROSITE, PS00041; C_Type_Lectin_2; 1.
 DR PROSITE, PS01186; EGF_2; 3.
 DR PROSITE, PS00026; EGF_3; 3.
 DR PROSITE, PS01187; EGF CA; 2.
 DR PROSITE, PS01187; EGF CA; 2.
 SQ SEQUENCE 577 AA; 61868 MW; B20E50BF8745014 CRC64;

Query Match 66.0%; Score 2113.5; DB 2; Length 577;
 Best Local Similarity 67.0%; Pred. No. 1,4e-131;
 Matches 388; Conservative 53; Mismatches 129; Indels 9; Gaps 5;
 QY 1 MGVVLGALALAGLPAPAPAPGSGSCVHEDECFALPYGPATFLNLSQICDGRGHL 60
 DB 1 MGVFLGLVLAAPASGLGALATLQPTGSCVHEGCFALFGGATFLDLSQACORLGHLM 60
 QY 61 TVRSSVAADVLSLINDG-GVGRRLWIGLQLPKCGDPRKLGPLRGQVWVTGNNTSY 119
 DB 61 TVRSSVAADVLSLINDG--WIGLQLPGCDPVLGFLRGQVWVTGNNHSY 117
 QY 120 SRMARLDNGAPLCPGLCVAVSAARATVPSEPIWEEQCEVADGFLCFEHPATCRPLA 179
 DB 118 SRMARPNQDTAPLCPGLCVATSTATEAAPGEPAWBEKCEETQGLCFEFTATSCRP 177
 QY 180 VEP-GAAAAVSYITGTFPAAGADFOALPVGSSAAVAPLGLQMLCTAPGAVQGHMWR 238
 DB 178 VMTRPBAAHISSTNTPTFGVSGADFOILPVGSSAAVEPLGLTLCRAAPGTSBGHME 237
 QY 239 APGAWDCSVENGCGEHCACNAIPGAPPCQAPAGALQADGRSCTAS-TQSCNDLCHEFCVP 297
 DB 238 ATGAWNCGSVENGCGEYLGNRSTNEPRCLCPRMMDLQADGRSARAVVSGNCLGHCFCVS 297
 QY 298 NPDPGASISCMCEITGYRLAADHREVDVDCILFESPCQRCVNTQGGRECHCYNYDLY 357
 DB 298 NAEVGSYSCEITGYQLAADHREVDVDCQKQGNPCPOLCVNTKGGRECHCYDGYEYLY 357
 QY 358 DGECEVAPDPCFRANCEYQCCPLNQTYSYLCVCAEGFAPRIPBPHRCOMFCNQTACPAD 417
 DB 358 DGECEVAPDPCFRANCEYQCCPLNQTYSYLCVCAEGFAPRIPBPHRCOMFCNQTACPAD 417
 QY 418 PNTQASCEPCBGYILDGFTCTDIDCENGFCGVCVCHNLPTGTECICGDPALARIHGT 477

DB 418 PMSFVCECPREFILDEGSCVCTDIDCEGCEFTBECNRPSPSYECICGDPALAGQISK 477
 QY 478 DCDGKVV--DCGDSGSGGPPSPPTPGSTLTPPAVLVGLGIGISLALCVVALLAL 534
 DB 478 DCDPFPVEDTBERGSGGPPSPPTPGSTLTPPAVLVGLGIGISLALCVVALLAL 537
 QY 535 LCHLRKKGAAARAKMEYKCAAPSKEVVLQHVTRTPTPR 573
 DB 538 LCHLRKKGAAARAELEYKCASSAKEVVLQHVTRDRLQK 576
 RESULT 8
 ID 035370 RAT PRELIMINARY; PRT; 577 AA.
 AC 035370;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
 DE Thrombomodulin.
 GN Name=Thbd;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RX MEDLINE=99246062; PubMed=10231031;
 RA Wang J., Yao A., Wang J.Y., Sung C.C., Fink L.M., Hardin J.W.,
 RA Hauer-Jensen M.,
 RT "cDNA cloning and sequencing, gene expression, and immunolocalization
 of thrombomodulin in the Sprague-Dawley rat.";
 RL DNA Res. 6:57-62(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Martina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casarini T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smallus D.E.,
 RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Straubeberg R.,
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF022743; AAB80760.1; -; mRNA.
 DR EMBL, BC070903; AAB70903.1; -; mRNA.
 DR HSSP, P07204; 1FGD.
 DR Ensembl, ENSRNOG0000004687; Rattus norvegicus.
 DR RGD, 621299; Thbd.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005509; F:calcium ion binding; IEA.
 DR GO, GO:0005529; F:sugar binding; IEA.
 DR GO, GO:0004888; F:transmembrane receptor activity; IEA.


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Db      312 EGFILDEGSICTDIDECSCQEGCLTNECRNPGSYECICGPTALAGQISKDCDIPVLEED 371
Qy      486 GGDGSGEPPPS-PTPGSTLTPPAVLVHSGLLIGISIAS/CLVVALALALCHLRKQGA 544
Db      372 SEDGSGSEHSSNTVVSSTVPSPAPMHSGLIGISIASLVALALALCHLRKQGT 431
Qy      545 ARAAMEYKCAPSKREVVLQHVTRTERTPQ 572
Db      432 ARAALEYKCTSSAKAEVLQHVTRTERLQ 459

RESULT 11
TRBM BOVIN
ID      TRBM BOVIN      STANDARD;      PRT;      356 AA.
AC      P06579;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Thrombomodulin (TM) (Fetomodulin) (Fragment).
GN      Name=THBD;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=87067408; PubMed=3024152;
RA      Jackson R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;
      "Characterization of a thrombomodulin cDNA reveals structural
      similarity to the low density lipoprotein receptor.";
      Proc. Natl. Acad. Sci. U.S.A. 83:8834-8838(1986).
CC      -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
      that forms a 1:1 stoichiometric complex with thrombin. This
      complex is responsible for the conversion of protein C to the
      activated protein C (protein Ca). Once evolved, protein Ca
      activates the activated cofactors of the coagulation mechanism,
      factor Va and factor VIII, and thereby reduces the amount of
      thrombin generated.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
      thrombomodulin.
CC      -1- SIMILARITY: Contains 6 EGF-like domains.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
      between the Swiss Institute of Bioinformatics and the EMBL outstation -
      the European Bioinformatics Institute. There are no restrictions on its
      use as long as its content is in no way modified and this statement is not
      removed.
CC      -----
CC      EMBL, M14657; AAA30785.1; -; mRNA.
CC      PIR, A25918; A25918.
CC      HSSP, P07204; 11MR.
CC      SMR, P06579; 137-253.
CC      InterPro, IPR000152; Asx hydroxyl_S.
CC      InterPro, IPR000742; EGF_2.
CC      InterPro, IPR001881; EGF_Ca bd.
CC      InterPro, IPR006209; EGF-like.
CC      InterPro, IPR001491; Thrombomodulin.
CC      Pfam, PF00008; EGF_2.
CC      Pfam, PF07645; EGF_CA_1.
CC      PRINTS, PR00907; THROMBOMODULIN.
CC      SMART, SM00179; EGF_CA_1.
CC      PROSITE, PS0010; ASX_HYDROXYL_2.
CC      PROSITE, PS00022; EGF_1; FALSE_NEG.
CC      PROSITE, PS01186; EGF_2; 3.
CC      PROSITE, PS50026; EGF_3; 3.
CC      PROSITE, PS01187; EGF_CA_2.
CC      Blood coagulation; EGF-like domain; Glycoprotein; Receptor; Repeat;
CC      Transmembrane.
KW      TOPO_DOM 1 296 Extracellular (Potential).
FT      TRANSMEM 297 320 Potential.
FT      TOPO_DOM 321 356 Cytoplasmic (Potential).

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FT      DOMAIN 17 57 EGF-like 1.
FT      DOMAIN 60 98 EGF-like 2.
FT      DOMAIN 99 137 EGF-like 3; calcium-binding (Potential).
FT      DOMAIN 139 179 EGF-like 4.
FT      DOMAIN 178 214 EGF-like 5.
FT      DOMAIN 215 254 EGF-like 6; calcium-binding (Potential).
FT      CARBOHYD 271 271 O-linked (Xyl. . .) (glycosaminoglycan) (By
FT      similarity).
FT      DISULFID 21 32 By similarity.
FT      DISULFID 28 41 By similarity.
FT      DISULFID 43 56 By similarity.
FT      DISULFID 64 72 By similarity.
FT      DISULFID 68 82 By similarity.
FT      DISULFID 84 97 By similarity.
FT      DISULFID 103 114 By similarity.
FT      DISULFID 110 123 By similarity.
FT      DISULFID 125 136 By similarity.
FT      DISULFID 143 152 By similarity.
FT      DISULFID 148 162 By similarity.
FT      DISULFID 164 178 By similarity.
FT      DISULFID 182 191 By similarity.
FT      DISULFID 187 199 By similarity.
FT      DISULFID 201 213 By similarity.
FT      DISULFID 219 228 By similarity.
FT      DISULFID 224 237 By similarity.
FT      DISULFID 239 253 By similarity.
FT      NON_TER 1 1
SQ      SEQUENCE 356 AA; 37795 MW; 29B41F097ABE1093 CRC64;

Query Match 41.0%; Score 1314; DB 1; Length 356;
Best Local Similarity 65.0%; Pred. No. 6.4e-79;
Matches 232; Conservative 42; Mismatches 67; Indels 16; Gaps 7;

Qy      229 GAVGSHARAEAPAGMDCSVENGCEHAENAIIPGAPPCCPAGALLOADRSC-TASTQSC 287
Db      5 GETGRSRREAPGAMACVVERGCGQHCKSGAGSNCLCPADALLOADRSCGPAEHPIC 64
Qy      288 NDLCENHFCVNPDPGYSKCEGTGYRIADQHRCEVDYDCILBSPPCQRCVNTQSGFE 347
Db      65 HOLCEHFC--HMHGIGNYTCICEAGYQLADQHRCEVDYDCIOLPSPCQRCVNTQSGFQ 122
Qy      348 CHCTPNTDLYNGCEVPPDPREFRANCEYCOPLNOTSYLCVCAGSFAPIPHEPRQWFC 407
Db      123 CHCTGVELVDGECVDPVPCFNNCEYCCQPVGRSEKCIICAGFAVPAAPHKQWFC 182
Qy      408 NOTACPADCDPNTQASCCEPGYILDQFICTDIDECENGGFCGVCNHLPTRECTICGP 467
Db      183 NOTSPADCDHYPTICPCPGYIIDEGSTCTDINEQDT-NICPGQCHNLPQTYECICGP 241
Qy      468 DSALARIHIGTDCDSGKV-----DGDGSGSGEPPPSPTPGSTLTP-PA-VGLVHSGLL 517
Db      242 DSALSGQIGIDCDPQVVERGTPEDYG--SGGEPPVSPTRGAVTARPSAPAGPLHSGVL 299
Qy      518 IGISIASICLVVALALALCHLRKQGAARAMEYKCAPSKREVVLQHVTRTERTPQL 574
Db      300 VGISIASISLVVALALALCHLRKQGSRGLEIKCVPAKELMLQGVKTERTPQKL 356

RESULT 12
Q4SWS2_TETNG PRELIMINARY; PRT; 496 AA.
ID      Q4SWS2_TETNG
AC      Q4SWS2;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Chromosome undetermined SCAFI3541, whole genome shotgun sequence.
GN      ORFNames=GSTENG00011332001;
OS      Tetraodon nigroviridis (Green puffer).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Necteleostei;
OC      Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC      Tetraodontidae; Tetraodontidae; Tetraodon.
OX      NCBI_TaxID=99883;

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RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fieber S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype." ;
 RL Nature 431:946-957(2004).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB0103541; CAF94910.1; -; Genomic DNA.
 SQ SEQUENCE 496 AA; 52663 MW; 1B270211A7A5C95A CRC64;
 Query Match 20.3%; Score 651.5; DB 2; Length 496;
 Best Local Similarity 35.1%; Pred. No. 5.7e-35;
 Matches 146; Conservative 40; Mismatches 143; Indels 87; Gaps 15;
 QY 24 QGGSCVCEHDCPLYPGPATFLNASQICDGLRGHMTVSSVADYISLLNGDGGYGR 83
 DB 23 KPSSGYCIGNOCFTASBQPTFVAQKECEGIGLMTVTSVSHDIVSLLGNVSG--- 79
 QY 84 RLWIGLQLPPCGCDPKRLGPFOWTGDNNNTSYSMARLDLNGAPLGCPLCYAVSAA 143
 DB 80 -RFMIGLPLTACDGSU--ELNGSWVPGESSEFSWMPAFAFGC--SSDRCVSVSPV 134
 QY 144 EATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAVEPAAAAAASITTYGTPFAARGAD 203
 DB 135 D-----PFKMTREPCDARAAGFLCFGNVTCRGL-----GAGAGTPTYSTPIGIEGGE 184
 QY 204 FQALPVSSAAVAPLGLQMLCTAPPGAVQGHMAREAPCAMDCSVENGCCEHACNAIPAR 263
 DB 185 LLSLPSPGVAALMPSGSKYIC-----PSGGWV-EAP--WTCEVLGGGCEHRCCTLDPRQM 235
 QY 264 P-CQCPAGAAAL-----OAGGRSCTASTOSCNULDCEHFCVNPDPDQSGSCMCETGY 313
 DB 236 PLCCPCPGQYTPENQVTCERAGDPCAAAR-----CAHACY--DNGSSHACKRGGF 286
 QY 314 RLAAOHRCEVDVDCILPSPPCORCVNTQGGFEGCHCYPNYDLVDGECVBEVDPCFRANC 373
 DB 287 KLAADGRSCVVDVDCV--SAPCEHCKKNSPGSYKACACSGY-RVDAAK----- 330
 QY 374 EYQCOPLNQSYLVCVCAEGFAPIPHEPRRCMFCNQTCAPADCDPNTQASCECEBG 429
 DB 331 -----EPHRCQLHCEBCECAACBQPRQVHLLRGG 361
 RESULT 13
 QATSR2_TETNG PRELIMINARY; PRT; 431 AA.
 AC QATSR2;
 DT 13-SEP-2005 (TREMblrel. 31, Created)
 DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
 DS Chromosome undetermined SCAF9151, whole genome shotgun sequence.
 DS (Fragment).
 GN ORFNames=STENG0006679001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fieber S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype." ;
 RL Nature 431:946-957(2004).
 RN
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01009151; CAF91770.1; -; Genomic DNA.
 FT NON TER 1 431
 FT NON TER 1 431
 SQ SEQUENCE 431 AA; 47647 MW; 7CCC872B307085A8 CRC64;
 Query Match 18.9%; Score 604.5; DB 2; Length 431;
 Best Local Similarity 33.2%; Pred. No. 6.4e-32;
 Matches 151; Conservative 49; Mismatches 182; Indels 73; Gaps 20;
 QY 30 CVEHDCPLYPGPATFLNASQICDGLRGHMTVSSVADYISLLNGDGGVRRRL-- 86
 DB 17 CTDDGCFWVHFQRTFLFESWRSCKDNGNGLAIIRKEDAGTIGRLFASADLRHSRTKQA 76
 QY 87 WIGLQL-PPCGCDPKRLGPFOWTGDNNNTSYSMARLDLNGAPLGCPLCYAVSAAEA 145
 DB 77 WIGLQHRHROCSATL---PLRGFSWTTGDDDTDTTMMGEGSPACL-APFCVAVV-YDA 131
 QY 146 TVPSEPI-WEEOCEVADGFLCEFHFPATCRPLAVEPAAAAAASITTYGTPFAARGAD 204
 DB 132 QKSDNLKMTVDGPCVAHTDGLCHYAVGCMPTLRSE-GAGKA---LYVPHLRSTLL 186
 QY 205 QALVVGSSAAV-APLGLQ---LMCTAPPGAVQGHMAREAPGA-----WDGSENGG 251
 DB 187 TLVPPGTVAATLPSPDTERESSVLTCTLRDDGL-ARWSRDQPFCSGPRVSRHM-CVDNNG 244
 QY 252 CEHACNAIPARPCQCPAGAAALQADGRSCTASTOSCNULDCEHFCVNPDPDQSGSCMCET 311
 DB 245 CEHFCRAAGVNPFCYCEBAGYQLAAGNQCCEPLDVCKSPCKFEELPISD---SYRCACP 301
 QY 312 GYRLAADOHRCEVDVDCILPSPPCORCVNTQGGFEGCHCYPNYDLVDGECVBEVDPCFR 370
 DB 302 GYMLAPBEHCDMDVDEL---QSPCEHLCVNSPSPGFERCBRGYLLDEGAC-ENADEGMA 358
 QY 371 ANCEYCOPLNQSYLVCVCAEGFAPIPHEPRRCMFCNQTCAPADCDPNTQASCECEBG 430
 DB 359 NPCEHACEN-TAGSHVCHGCELGFEPIEDPSRCQ----- 391
 QY 431 ILDDGFLCTDIDCEENGGPSCGVCHNLPTFFECTC 465
 DB 392 -----DTDECRMAGTCCQICVNFEGSFQCYC 417
 RESULT 14
 OS9EB6_HUMAN
 ID OS9EB6_HUMAN PRELIMINARY; PRT; 671 AA.
 AC OS9EB6;

DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Complement component 1, q subcomponent, receptor 1 variant
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Aorta endothelial cell;
 RA Totsuki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
 RA Ohara O., Nagase T., Kikuno F.R.;
 RA "None Title."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB209895; BAD93132.1; -, mRNA.
 DR Ensembl; ENSG00000125810; Homo sapiens.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca bd.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF07645; EGF_CA; 3.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 5.
 DR SMART; SM00179; EGF_CA; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR Receptor.
 KW NON TER.
 FT
 SQ SEQUENCE 671 AA; 70460 MW; 00CDB6C5EAB63 CRC64;
 Query Match 18.6%; Score 597; DB 2; Length 671;
 Best Local Similarity 30.9%; Pred. No. 3.1e-31;
 Matches 181; Conservative 54; Mismatches 205; Indels 146; Gaps 31;
 QY 12 LAGGFPAAR-----PQSGSQ-----CNEHDCFALYRGP 42
 DB 3 LSPGFSPBAGHETETGNATSMGLLLLLLTTPGAGTADTEAVVCGTACTYAHSGK 62
 QY 43 ATPFNASQICDGLRHLMTVRSSVAAD---VISLLNGDGVGR--RLWTLQLPPG- 95
 DB 63 LSAEAHQHCHONONGENLITVSKERAYQVRLAQLRLBAALTARMKRFNIGLQREKQ 122
 QY 96 CGDPRRLPLNGFQWVTGDNNTSYSRMARLDLNGAPLGCPLVA--VSAEAETVSE-PI 152
 DB 123 CLDPSL--PLKGFSSVVGGEDETPYGNMHEKLNESC--ISKRCVSLLDLSQPLRSRLPK 178
 QY 153 WEEQOC-----EYKADGFLCEFHNPATCRPLAV-EPGAAAASVITGTPPAAGADPQ 205
 DB 179 WSEGGCGSPGSPGSIIEGVCFKFSFKGCRPLALGPG-----QVYTTPTPQTSSSLE 232
 QY 206 ALPVSSAAVAPLGIQLMC--TAPGAVQGHM---ARAPGAMD-----CSV 247
 DB 233 AVFPASANVA-----CGBEDKDETQSHYFLCKEKADVDVWQSSGELCVSPRYGCVF 285
 QY 248 ENGGEHAC-NAIPGAPCCQAGALQADRSCTASTOSCNLDCE--HFCVNPDPQGS 304
 DB 286 NNGGCHQCFCBGDSDSLGCRPRRLDDVLVTSARNPCSSPFGAGTCLG-NGKN 344
 QY 305 YSCMCETGYRLAADHRCEDVDCLLEBPSPQRCQVNTQSGECGCHYENYDLVDGCVEP 364

DB 345 YTCRCPGCYQLDSQDLCDVDEEC--QDSPCAQECVNTPGFRCCEWVG-----EP 394
 QY 365 VDPCEFRANCEYOCPLNQTSTLCYCAEGFAPIPHEPRCOMFCNQTACPADCDNTQAS- 423
 DB 395 GGF-----GGGACQDVDE-----CALGRSP-----CAQGC-TNTDGSF 426
 QY 424 -CECPGGYIL--DDGFICTDIDEC--ENGFCSCVCHNLGTFECTICGPDLSALARIHGTD 478
 DB 427 HSCSEEGYVLAGEBDGTQCODVDECVGPGGLCSTLCNTGSSFFQGLPGWVLAPN-GVS 485
 QY 479 CDGSKV-----DGDGSGSG-----PPSPPTGSLTPPA 508
 DB 486 CTWGPVSLGPPSGPPDEEDKSEKSGTVPPRAATSPTRGEGTPKA 531
 RESULT 15
 ID CIGRI_HUMAN STANDARD; PRT; 652 AA.
 AC Q9NPY3; Q00274;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Complement component C1q receptor precursor (Complement component 1, q subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor) (CD93 antigen) (CDW93).
 DE (CD93 antigen) (CDW93).
 GN Name=C1QR1; Synonyms=CD93;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN
 RX MEDLINE=97199258; PubMed=9047234; DOI=10.1016/S1074-7613(00)80419-7;
 RX Neomunceno R.R., Henschel-Bdman A.H., Burgess W.H., Temner A.J.,
 RX "cDNA cloning and primary structure analysis of C1qR(p), the human
 RX C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro."
 RX Immunity 6:119-129(1997).
 RN
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-318.
 RX MEDLINE=21640567; PubMed=11781389;
 RX Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
 RX Prager E., Staefler G., Madic O., Stockinger H., Knapp W.;
 RX "Identification of human CD93 as the phagocytic C1q receptor (C1qR)
 RX by expression cloning."
 RX J. Leukoc. Biol. 71:133-140(2002).
 RN
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RX Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
 RX Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RX Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RX Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RX Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RX Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
 RX Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RX Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RX Grahame D.V., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RX Hammond E., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,
 RX Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RX Kay M.P., Kimberley A.W., King A., Knights K., Laird G.K., Lawlor S.,
 RX Lehaealaih M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RX Marsh V.L., Martin S.L., McConachie L.J., McLeay K., Murray A.A.,
 RX Mlyn S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RX Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RX Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
 RX Rice C.M., Ross M.T., Scott C.B., Senta H.K., Showkeen R., Sims S.,
 RX Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.B.,
 RX Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RX Tracey A., Tromans A.C., Taylor M., Wall M., Wallis J.M.,
 RX Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RX Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=leukocyte;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaltus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RN CHARACTERIZATION.
 RP MEDLINE=21990337; PubMed=11994479;
 RX McCreel E.P., Ikewaki N., Akatsu H., Morgan B.P., Gaege P.;
 RT "Human C1qR is identical with CD93 and the mH-11 antigen but does
 not bind C1q.";
 RT J. Immunol. 168:5222-5232(2002).
 RN [6]
 RP O-GLYCOSYLATION.
 RX MEDLINE=99192777; PubMed=10092817; Tenner A.J.;
 RA Nepomuceno R.R., Ruiz S., Park M.,
 RT "C1qR is a heavily O-glycosylated cell surface protein involved in
 the regulation of phagocytic activity.";
 RL J. Immunol. 162:3583-3589(1999).
 RN [7]
 RP INTERACTION WITH HCV CORE PROTEIN.
 RX PubMed=11086025;
 RA Kittlesen D.J., Chianese-Bullock K.A., Yao Z.Q., Braciare T.J.,
 RA Hahn Y.S.;
 RT "Interaction between complement receptor gC1qR and hepatitis C virus
 core protein inhibits T-lymphocyte proliferation.";
 RL J. Clin. Invest. 106:1239-1249(2000).
 CC -1- FUNCTION: Receptor (or element of a larger receptor complex) for
 C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
 protein A (SPA). May mediate the enhancement of phagocytosis in
 monocytes and macrophages upon interaction with soluble defense
 collagens. May play a role in intercellular adhesion.
 CC -1- SUBUNIT: Interacts with HCV core protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
 platelets, cells of myeloid origin, such as monocytes and
 neutrophils. Not expressed in cells of lymphoid origin.
 CC -1- PTM: N- and O-glycosylated.
 CC -1- SIMILARITY: Contains 1 C-type lectin domain.
 CC -1- SIMILARITY: Contains 5 EGF-like domains.
 CC -1- CAUTION: Has been sometimes referred to as a collectin receptor.
 CC -1- CAUTION: Ref.5 reported that C1q is not a ligand for C1QRI.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; U94333; AAB53110.1; -; mRNA.
 DR EMBL; AL118508; CAC00597.1; -; Genomic DNA.

DR EMBL; BC028075; AAB28075.1; -; mRNA.
 DR HSSP; P35555; IEMN.
 DR Ensembl; ENSG00000125810; Homo sapiens.
 DR HGNC; HGNC:15855; C1QRI.
 DR H-InvDB; HIX0015687; -.
 DR MIM; 120577; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006960; P:antimicrobial humoral response (sensu Proto. . .; TAS.
 DR GO; GO:0016337; P:cell-cell adhesion; IDA.
 DR GO; GO:0042116; P:macrophage activation; NAS.
 DR GO; GO:0006909; P:phagocytosis; NAS.
 DR InterPro; IPR000152; ASX hydroxyl_S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF Ca bd.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR01304; Lectin_C.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF07645; EGF_CA; 3.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; C1QRT; 1.
 DR SMART; SM00179; EGF_CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3. FALSE_NEG.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR Cell adhesion; Direct protein sequencing; EGF-like domain;
 KW Glycoprotein; Lectin; Polymorphism; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 652
 FT TOPO_DOM 22 580
 FT TRANSMEM 581 601
 FT TOPO_DOM 602 652
 FT DOMAIN 32 174
 FT DOMAIN 260 301
 FT DOMAIN 302 344
 FT DOMAIN 345 384
 FT DOMAIN 385 426
 FT DOMAIN 427 468
 FT DOMAIN 494 601
 FT CARBOHYD 325 325
 FT DISULFID 264 275
 FT DISULFID 271 285
 FT DISULFID 287 300
 FT DISULFID 306 317
 FT DISULFID 311 328
 FT DISULFID 330 343
 FT DISULFID 349 358
 FT DISULFID 354 367
 FT DISULFID 369 383
 FT DISULFID 389 400
 FT DISULFID 396 409
 FT DISULFID 411 425
 FT DISULFID 431 443
 FT DISULFID 439 452
 FT DISULFID 454 467
 FT VARIANT 318 318
 FT CONFLICT 22 22 /Prid=VAR_013573.
 FT CONFLICT 36 36 T->V (in Ref. 1; AA sequence).
 FT CONFLICT 39 39 C->T (in Ref. 1; AA sequence).
 FT CONFLICT 155 155 TA->N (in Ref. 1; AA sequence).
 FT CONFLICT 186 186 S->N (in Ref. 1).
 FT CONFLICT 186 186 G->A (in Ref. 1; AA sequence).
 FT CONFLICT 492 492 S->A (in Ref. 1; AA sequence).
 FT CONFLICT 496 496 R->Q (in Ref. 1; AA sequence).
 FT CONFLICT 504 504 R->G (in Ref. 1; AA sequence).
 FT CONFLICT 541 541 P->S (in Ref. 1).
 Query Match 18.4%; Score 590.5; DB 1; Length 652;

